

SEQUENCE LISTING



(1) GENERAL INFORMATION

(i) APPLICANT: Summers, Neena
McWherter, Charles
Feng, Yiqing

(ii) TITLE OF THE INVENTION: Novel Erythropoietin Receptor
Agonists

(iii) NUMBER OF SEQUENCES: 135

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: G. D. Searle & Co.
(B) STREET: P.O. Box 5110
(C) CITY: Chicago
(D) STATE: IL
(E) COUNTRY: U. S. A.
(F) ZIP: 60680

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/954,954
(B) FILING DATE: 21-OCT-1997
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 60/034,044
(B) FILING DATE: 25-OCT-1996

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Bennett, Dennis A
(B) REGISTRATION NUMBER: 34,547
(C) REFERENCE/DOCKET NUMBER: 2991/1

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 314-737-6986
(B) TELEFAX: 314-737-6972
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 170 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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GROUP 1700*AK*

Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu Asn Ile
 1 5 10 15
 Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg Met Glu
 20 25 30
 Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu Leu Ser
 35 40 45
 Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser Gln Pro
 50 55 60
 Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly Leu Arg
 65 70 75 80
 Ser Leu Thr Thr Leu Arg Ala Leu Gly Ala Gln Lys Glu Ala Ile
 85 90 95
 Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala
 100 105 110
 Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly
 115 120 125
 Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp Arg Gly
 130 135 140
 Gly Gly Ser Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu
 145 150 155 160
 Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu
 165 170

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu Asn Ile Thr
 1 5 10 15
 Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val
 20 25 30
 Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu Leu Ser Glu
 35 40 45
 Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser Gln Pro Trp
 50 55 60
 Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly Leu Arg Ser
 65 70 75 80
 Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu Ala Ile Ser
 85 90 95
 Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp
 100 105 110
 Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys
 115 120 125
 Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp Arg Gly Gly
 130 135 140
 Gly Ser Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg
 145 150 155 160
 Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn
 165 170

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
 (B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val
1 5 10 15
Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly
20 25 30
Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala
35 40 45
Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser Gln Pro Trp Glu
50 55 60
Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly Leu Arg Ser Leu
65 70 75 80
Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu Ala Ile Ser Pro
85 90 95
Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr
100 105 110
Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu
115 120 125
Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp Arg Gly Gly Gly
130 135 140
Ser Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr
145 150 155 160
Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile
165 170

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 170 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val Pro
1 5 10 15
Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly Gln
20 25 30
Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val
35 40 45
Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser Gln Pro Trp Glu Pro
50 55 60
Leu Gln Leu His Val Asp Lys Ala Val Ser Gly Leu Arg Ser Leu Thr
65 70 75 80
Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro
85 90 95
Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe
100 105 110
Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys
115 120 125
Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp Arg Gly Gly Gly Ser
130 135 140
Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu
145 150 155 160
Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr

165

170


(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:



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Gly Cys Ala Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp
 1      5      10      15
Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln
      20      25      30
Ala Val Glu Val Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu
      35      40      45
Arg Gly Gln Ala Leu Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu
      50      55      60
Gln Leu His Val Asp Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr
      65      70      75      80
Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp
      85      90      95
Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg
      100      105      110
Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu
      115      120      125
Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp Arg Gly Gly Gly Ser Ala
      130      135      140
Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu
      145      150      155      160
Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr
      165      170

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(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

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Cys Ala Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr
 1      5      10      15
Lys Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala
      20      25      30
Val Glu Val Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg
      35      40      45
Gly Gln Ala Leu Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln
      50      55      60
Leu His Val Asp Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu
      65      70      75      80
Leu Arg Ala Leu Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala
      85      90      95
Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys
      100      105      110

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Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr
 115 120 125
 Thr Gly Glu Ala Cys Arg Thr Gly Asp Arg Gly Gly Gly Ser Ala Pro
 130 135 140
 Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu
 145 150 155 160
 Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly
 165 170


(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:



Ala Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys
 1 5 10 15
 Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val
 20 25 30
 Glu Val Trp Gln Gly Leu Ala Leu Ser Glu Ala Val Leu Arg Gly
 35 40 45
 Gln Ala Leu Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu
 50 55 60
 His Val Asp Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu
 65 70 75 80
 Arg Ala Leu Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala
 85 90 95
 Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu
 100 105 110
 Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr
 115 120 125
 Gly Glu Ala Cys Arg Thr Gly Asp Arg Gly Gly Gly Ser Ala Pro Pro
 130 135 140
 Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala
 145 150 155 160
 Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys
 165 170

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val
 1 5 10 15
 Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu
 20 25 30
 Val Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln
 35 40 45
 Ala Leu Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His

50 55 60
Val Asp Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg
65 70 75 80
Ala Leu Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser
85 90 95
Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe
100 105 110
Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly
115 120 125
Glu Ala Cys Arg Thr Gly Asp Arg Gly Gly Gly Ser Ala Pro Pro Arg
130 135 140
Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys
145 150 155 160
Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala
165 170

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

His Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn
1 5 10 15
Phe Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val
20 25 30
Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala
35 40 45
Leu Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val
50 55 60
Asp Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala
65 70 75 80
Leu Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala
85 90 95
Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg
100 105 110
Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu
115 120 125
Ala Cys Arg Thr Gly Asp Arg Gly Gly Gly Ser Ala Pro Pro Arg Leu
130 135 140
Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu
145 150 155 160
Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu
165 170

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe
 1 5 10 15
 Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp
 20 25 30
 Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu
 35 40 45
 Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp
 50 55 60
 Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu
 65 70 75 80
 Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala
 85 90 95
 Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val
 100 105 110
 Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala
 115 120 125
 Cys Arg Thr Gly Asp Arg Gly Gly Gly Ser Ala Pro Pro Arg Leu Ile
 130 135 140
 Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala
 145 150 155 160
 Glu Asn Ile Thr Thr Gly Cys Ala Glu His
 165 170

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr
 1 5 10 15
 Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln
 20 25 30
 Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu
 35 40 45
 Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys
 50 55 60
 Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly
 65 70 75 80
 Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro
 85 90 95
 Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr
 100 105 110
 Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys
 115 120 125
 Arg Thr Gly Asp Arg Gly Gly Gly Ser Ala Pro Pro Arg Leu Ile Cys
 130 135 140
 Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu
 145 150 155 160
 Asn Ile Thr Thr Gly Cys Ala Glu His Cys
 165 170

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
 (B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala
1 5 10 15
Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly
20 25 30
Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val
35 40 45
Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala
50 55 60
Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala
65 70 75 80
Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu
85 90 95
Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser
100 105 110
Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg
115 120 125
Thr Gly Asp Arg Gly Gly Gly Ser Ala Pro Pro Arg Leu Ile Cys Asp
130 135 140
Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn
145 150 155 160
Ile Thr Thr Gly Cys Ala Glu His Cys Ser
165 170

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 170 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp
1 5 10 15
Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu
20 25 30
Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn
35 40 45
Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val
50 55 60
Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln
65 70 75 80
Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg
85 90 95
Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn
100 105 110
Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr
115 120 125
Gly Asp Arg Gly Gly Gly Ser Ala Pro Pro Arg Leu Ile Cys Asp Ser
130 135 140
Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile
145 150 155 160
Thr Thr Gly Cys Ala Glu His Cys Ser Leu

165

170

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys
 1 5 10 15
 Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala
 20 25 30
 Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser
 35 40 45
 Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser
 50 55 60
 Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys
 65 70 75 80
 Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr
 85 90 95
 Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe
 100 105 110
 Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly
 115 120 125
 Asp Arg Gly Gly Gly Ser Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg
 130 135 140
 Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr
 145 150 155 160
 Thr Gly Cys Ala Glu His Cys Ser Leu Asn
 165 170

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg
 1 5 10 15
 Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu
 20 25 30
 Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser
 35 40 45
 Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly
 50 55 60
 Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu
 65 70 75 80
 Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile
 85 90 95
 Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu
 100 105 110

Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp
 115 120 125
 Arg Gly Gly Gly Ser Ala Pro Arg Leu Ile Cys Asp Ser Arg Val
 130 135 140
 Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr
 145 150 155 160
 Gly Cys Ala Glu His Cys Ser Leu Asn Glu
 165 170

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg Met
 1 5 10 15
 Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu Leu
 20 25 30
 Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser Gln
 35 40 45
 Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly Leu
 50 55 60
 Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu Ala
 65 70 75 80
 Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr
 85 90 95
 Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg
 100 105 110
 Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp Arg
 115 120 125
 Gly Gly Gly Ser Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu
 130 135 140
 Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly
 145 150 155 160
 Cys Ala Glu His Cys Ser Leu Asn Glu Asn
 165 170

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val
 1 5 10 15
 Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu Leu Ser Glu
 20 25 30
 Ala Val Leu Arg Gly Gln Ala Leu Val Asn Ser Ser Gln Pro Trp
 35 40 45
 Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly Leu Arg Ser

50 55 60
 Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu Ala Ile Ser
 65 70 75 80
 Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp
 85 90 95
 Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys
 100 105 110
 Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp Arg Gly Gly
 115 120 125
 Gly Ser Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg
 130 135 140
 Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala
 145 150 155 160
 Glu His Cys Ser Leu Asn Glu Asn Ile Thr
 165 170

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly
 1 5 10 15
 Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala
 20 25 30
 Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser Gln Pro Trp Glu
 35 40 45
 Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly Leu Arg Ser Leu
 50 55 60
 Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu Ala Ile Ser Pro
 65 70 75 80
 Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr
 85 90 95
 Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu
 100 105 110
 Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp Arg Gly Gly Gly
 115 120 125
 Ser Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr
 130 135 140
 Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu
 145 150 155 160
 His Cys Ser Leu Asn Glu Asn Ile Thr Val
 165 170

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly Gln
 1 5 10 15
 Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val
 20 25 30
 Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser Gln Pro Trp Glu Pro
 35 40 45
 Leu Gln Leu His Val Asp Lys Ala Val Ser Gly Leu Arg Ser Leu Thr
 50 55 60
 Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro
 65 70 75 80
 Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe
 85 90 95
 Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys
 100 105 110
 Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp Arg Gly Gly Gly Ser
 115 120 125
 Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu
 130 135 140
 Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His
 145 150 155 160
 Cys Ser Leu Asn Glu Asn Ile Thr Val Pro
 165 170

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala
 1 5 10 15
 Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser
 20 25 30
 Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser
 35 40 45
 Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys
 50 55 60
 Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr
 65 70 75 80
 Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe
 85 90 95
 Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly
 100 105 110
 Asp Arg Gly Gly Gly Ser Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg
 115 120 125
 Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr
 130 135 140
 Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val Pro
 145 150 155 160
 Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys
 165 170

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
 (B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu
1 5 10 15
Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser
20 25 30
Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly
35 40 45
Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu
50 55 60
Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile
65 70 75 80
Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu
85 90 95
Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp
100 105 110
Arg Gly Gly Gly Ser Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val
115 120 125
Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr
130 135 140
Gly Cys Ala Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp
145 150 155 160
Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg
165 170

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 170 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu Leu
1 5 10 15
Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser Gln
20 25 30
Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly Leu
35 40 45
Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu Ala
50 55 60
Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr
65 70 75 80
Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg
85 90 95
Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp Arg
100 105 110
Gly Gly Gly Ser Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu
115 120 125
Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly
130 135 140
Cys Ala Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr
145 150 155 160
Lys Val Asn Phe Tyr Ala Trp Lys Arg Met

165

170

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu Leu Ser
 1 5 10 15
 Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser Gln Pro
 20 25 30
 Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly Leu Arg
 35 40 45
 Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu Ala Ile
 50 55 60
 Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala
 65 70 75 80
 Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly
 85 90 95
 Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp Arg Gly
 100 105 110
 Gly Gly Ser Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu
 115 120 125
 Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys
 130 135 140
 Ala Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys
 145 150 155 160
 Val Asn Phe Tyr Ala Trp Lys Arg Met Glu
 165 170

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Gln Ala Leu Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu
 1 5 10 15
 His Val Asp Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu
 20 25 30
 Arg Ala Leu Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala
 35 40 45
 Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu
 50 55 60
 Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr
 65 70 75 80
 Gly Glu Ala Cys Arg Thr Gly Asp Arg Gly Gly Gly Ser Ala Pro Pro
 85 90 95
 Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala
 100 105 110

Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu
 115 120 125
 Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp
 130 135 140
 Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu
 145 150 155 160
 Ala Leu Leu Ser Glu Ala Val Leu Arg Gly
 165 170

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Ala Leu Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His
 1 5 10 15
 Val Asp Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg
 20 25 30
 Ala Leu Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser
 35 40 45
 Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe
 50 55 60
 Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly
 65 70 75 80
 Glu Ala Cys Arg Thr Gly Asp Arg Gly Gly Ser Ala Pro Pro Arg
 85 90 95
 Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys
 100 105 110
 Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn
 115 120 125
 Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys
 130 135 140
 Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala
 145 150 155 160
 Leu Leu Ser Glu Ala Val Leu Arg Gly Gln
 165 170

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Leu Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val
 1 5 10 15
 Asp Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala
 20 25 30
 Leu Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala
 35 40 45
 Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg

50 55 60
 Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu
 65 70 75 80
 Ala Cys Arg Thr Gly Asp Arg Gly Gly Gly Ser Ala Pro Pro Arg Leu
 85 90 95
 Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu
 100 105 110
 Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu
 115 120 125
 Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg
 130 135 140
 Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu
 145 150 155 160
 Leu Ser Glu Ala Val Leu Arg Gly Gln Ala
 165 170

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp
 1 5 10 15
 Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu
 20 25 30
 Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala
 35 40 45
 Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val
 50 55 60
 Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala
 65 70 75 80
 Cys Arg Thr Gly Asp Arg Gly Gly Gly Ser Ala Pro Pro Arg Leu Ile
 85 90 95
 Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala
 100 105 110
 Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu Asn
 115 120 125
 Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg Met
 130 135 140
 Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu Leu
 145 150 155 160
 Ser Glu Ala Val Leu Arg Gly Gln Ala Leu
 165 170

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys
 1 5 10 15
 Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly
 20 25 30
 Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro
 35 40 45
 Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr
 50 55 60
 Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys
 65 70 75 80
 Arg Thr Gly Asp Arg Gly Gly Gly Ser Ala Pro Pro Arg Leu Ile Cys
 85 90 95
 Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu
 100 105 110
 Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu Asn Ile
 115 120 125
 Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg Met Glu
 130 135 140
 Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu Leu Ser
 145 150 155 160
 Glu Ala Val Leu Arg Gly Gln Ala Leu Leu
 165 170

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala
 1 5 10 15
 Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala
 20 25 30
 Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu
 35 40 45
 Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser
 50 55 60
 Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg
 65 70 75 80
 Thr Gly Asp Arg Gly Gly Gly Ser Ala Pro Pro Arg Leu Ile Cys Asp
 85 90 95
 Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn
 100 105 110
 Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu Asn Ile Thr
 115 120 125
 Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val
 130 135 140
 Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu Leu Ser Glu
 145 150 155 160
 Ala Val Leu Arg Gly Gln Ala Leu Leu Val
 165 170

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
 (B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val
 1 5 10 15
 Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln
 20 25 30
 Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg
 35 40 45
 Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn
 50 55 60
 Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr
 65 70 75 80
 Gly Asp Arg Gly Gly Ser Ala Pro Pro Arg Leu Ile Cys Asp Ser
 85 90 95
 Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile
 100 105 110
 Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val
 115 120 125
 Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly
 130 135 140
 Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala
 145 150 155 160
 Val Leu Arg Gly Gln Ala Leu Leu Val Asn
 165 170

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 170 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser
 1 5 10 15
 Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys
 20 25 30
 Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr
 35 40 45
 Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe
 50 55 60
 Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly
 65 70 75 80
 Asp Arg Gly Gly Gly Ser Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg
 85 90 95
 Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr
 100 105 110
 Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val Pro
 115 120 125
 Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly Gln
 130 135 140
 Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val
 145 150 155 160
 Leu Arg Gly Gln Ala Leu Leu Val Asn Ser

165

170


(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:



Gln	Pro	Trp	Glu	Pro	Leu	Gln	Leu	His	Val	Asp	Lys	Ala	Val	Ser	Gly
1				5					10					15	
Leu	Arg	Ser	Leu	Thr	Thr	Leu	Leu	Arg	Ala	Leu	Gly	Ala	Gln	Lys	Glu
			20					25					30		
Ala	Ile	Ser	Pro	Pro	Asp	Ala	Ala	Ser	Ala	Ala	Pro	Leu	Arg	Thr	Ile
		35					40					45			
Thr	Ala	Asp	Thr	Phe	Arg	Lys	Leu	Phe	Arg	Val	Tyr	Ser	Asn	Phe	Leu
	50					55					60				
Arg	Gly	Lys	Leu	Lys	Leu	Tyr	Thr	Gly	Glu	Ala	Cys	Arg	Thr	Gly	Asp
65					70				75					80	
Arg	Gly	Gly	Gly	Ser	Ala	Pro	Pro	Arg	Leu	Ile	Cys	Asp	Ser	Arg	Val
				85					90					95	
Leu	Glu	Arg	Tyr	Leu	Leu	Glu	Ala	Lys	Glu	Ala	Glu	Asn	Ile	Thr	Thr
			100					105					110		
Gly	Cys	Ala	Glu	His	Cys	Ser	Leu	Asn	Glu	Asn	Ile	Thr	Val	Pro	Asp
		115					120					125			
Thr	Lys	Val	Asn	Phe	Tyr	Ala	Trp	Lys	Arg	Met	Glu	Val	Gly	Gln	Gln
	130					135					140				
Ala	Val	Glu	Val	Trp	Gln	Gly	Leu	Ala	Leu	Leu	Ser	Glu	Ala	Val	Leu
145					150					155					160
Arg	Gly	Gln	Ala	Leu	Leu	Val	Asn	Ser	Ser						
				165					170						

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Pro	Trp	Glu	Pro	Leu	Gln	Leu	His	Val	Asp	Lys	Ala	Val	Ser	Gly	Leu
1				5					10					15	
Arg	Ser	Leu	Thr	Thr	Leu	Leu	Arg	Ala	Leu	Gly	Ala	Gln	Lys	Glu	Ala
			20					25					30		
Ile	Ser	Pro	Pro	Asp	Ala	Ala	Ser	Ala	Ala	Pro	Leu	Arg	Thr	Ile	Thr
		35					40					45			
Ala	Asp	Thr	Phe	Arg	Lys	Leu	Phe	Arg	Val	Tyr	Ser	Asn	Phe	Leu	Arg
	50					55				60					
Gly	Lys	Leu	Lys	Leu	Tyr	Thr	Gly	Glu	Ala	Cys	Arg	Thr	Gly	Asp	Arg
65					70					75				80	
Gly	Gly	Gly	Ser	Ala	Pro	Pro	Arg	Leu	Ile	Cys	Asp	Ser	Arg	Val	Leu
			85						90					95	
Glu	Arg	Tyr	Leu	Leu	Glu	Ala	Lys	Glu	Ala	Glu	Asn	Ile	Thr	Thr	Gly
			100					105					110		

Cys Ala Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr
 115 120 125
 Lys Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala
 130 135 140
 Val Glu Val Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg
 145 150 155 160
 Gly Gln Ala Leu Leu Val Asn Ser Ser Gln
 165 170

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly Leu Arg
 1 5 10 15
 Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu Ala Ile
 20 25 30
 Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala
 35 40 45
 Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly
 50 55 60
 Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp Arg Gly
 65 70 75 80
 Gly Gly Ser Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu
 85 90 95
 Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys
 100 105 110
 Ala Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys
 115 120 125
 Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val
 130 135 140
 Glu Val Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly
 145 150 155 160
 Gln Ala Leu Leu Val Asn Ser Ser Gln Pro
 165 170

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly Leu Arg Ser
 1 5 10 15
 Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu Ala Ile Ser
 20 25 30
 Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp
 35 40 45
 Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys

50 55 60
 Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp Arg Gly Gly
 65 70 75 80
 Gly Ser Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg
 85 90 95
 Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala
 100 105 110
 Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val
 115 120 125
 Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu
 130 135 140
 Val Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln
 145 150 155 160
 Ala Leu Leu Val Asn Ser Ser Gln Pro Trp
 165 170

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Leu Arg Ala Leu Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala
 1 5 10 15
 Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys
 20 25 30
 Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr
 35 40 45
 Thr Gly Glu Ala Cys Arg Thr Gly Asp Arg Gly Gly Gly Ser Ala Pro
 50 55 60
 Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu
 65 70 75 80
 Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser
 85 90 95
 Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala
 100 105 110
 Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly
 115 120 125
 Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val
 130 135 140
 Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala
 145 150 155 160
 Val Ser Gly Leu Arg Ser Leu Thr Thr Leu
 165 170

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Arg Ala Leu Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala
 1 5 10 15
 Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu
 20 25 30
 Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr
 35 40 45
 Gly Glu Ala Cys Arg Thr Gly Asp Arg Gly Gly Gly Ser Ala Pro Pro
 50 55 60
 Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala
 65 70 75 80
 Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu
 85 90 95
 Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp
 100 105 110
 Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu
 115 120 125
 Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn
 130 135 140
 Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val
 145 150 155 160
 Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu
 165 170

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Ala Leu Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser
 1 5 10 15
 Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe
 20 25 30
 Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly
 35 40 45
 Glu Ala Cys Arg Thr Gly Asp Arg Gly Gly Gly Ser Ala Pro Pro Arg
 50 55 60
 Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys
 65 70 75 80
 Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn
 85 90 95
 Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys
 100 105 110
 Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala
 115 120 125
 Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser
 130 135 140
 Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser
 145 150 155 160
 Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg
 165 170

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
 (B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Leu	Gly	Ala	Gln	Lys	Glu	Ala	Ile	Ser	Pro	Pro	Asp	Ala	Ala	Ser	Ala
1				5					10					15	
Ala	Pro	Leu	Arg	Thr	Ile	Thr	Ala	Asp	Thr	Phe	Arg	Lys	Leu	Phe	Arg
			20					25					30		
Val	Tyr	Ser	Asn	Phe	Leu	Arg	Gly	Lys	Leu	Lys	Leu	Tyr	Thr	Gly	Glu
		35					40					45			
Ala	Cys	Arg	Thr	Gly	Asp	Arg	Gly	Gly	Gly	Ser	Ala	Pro	Pro	Arg	Leu
	50					55					60				
Ile	Cys	Asp	Ser	Arg	Val	Leu	Glu	Arg	Tyr	Leu	Leu	Glu	Ala	Lys	Glu
65					70					75				80	
Ala	Glu	Asn	Ile	Thr	Thr	Gly	Cys	Ala	Glu	His	Cys	Ser	Leu	Asn	Glu
			85						90					95	
Asn	Ile	Thr	Val	Pro	Asp	Thr	Lys	Val	Asn	Phe	Tyr	Ala	Trp	Lys	Arg
			100					105					110		
Met	Glu	Val	Gly	Gln	Gln	Ala	Val	Glu	Val	Trp	Gln	Gly	Leu	Ala	Leu
		115					120					125			
Leu	Ser	Glu	Ala	Val	Leu	Arg	Gly	Gln	Ala	Leu	Leu	Val	Asn	Ser	Ser
	130					135					140				
Gln	Pro	Trp	Glu	Pro	Leu	Gln	Leu	His	Val	Asp	Lys	Ala	Val	Ser	Gly
145					150					155					160
Leu	Arg	Ser	Leu	Thr	Thr	Leu	Leu	Arg	Ala						
				165					170						

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 170 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Gly	Ala	Gln	Lys	Glu	Ala	Ile	Ser	Pro	Pro	Asp	Ala	Ala	Ser	Ala	Ala
1				5					10					15	
Pro	Leu	Arg	Thr	Ile	Thr	Ala	Asp	Thr	Phe	Arg	Lys	Leu	Phe	Arg	Val
			20					25					30		
Tyr	Ser	Asn	Phe	Leu	Arg	Gly	Lys	Leu	Lys	Leu	Tyr	Thr	Gly	Glu	Ala
		35					40					45			
Cys	Arg	Thr	Gly	Asp	Arg	Gly	Gly	Gly	Ser	Ala	Pro	Pro	Arg	Leu	Ile
	50					55					60				
Cys	Asp	Ser	Arg	Val	Leu	Glu	Arg	Tyr	Leu	Leu	Glu	Ala	Lys	Glu	Ala
65					70					75				80	
Glu	Asn	Ile	Thr	Thr	Gly	Cys	Ala	Glu	His	Cys	Ser	Leu	Asn	Glu	Asn
			85						90					95	
Ile	Thr	Val	Pro	Asp	Thr	Lys	Val	Asn	Phe	Tyr	Ala	Trp	Lys	Arg	Met
			100					105					110		
Glu	Val	Gly	Gln	Gln	Ala	Val	Glu	Val	Trp	Gln	Gly	Leu	Ala	Leu	Leu
		115					120					125			
Ser	Glu	Ala	Val	Leu	Arg	Gly	Gln	Ala	Leu	Leu	Val	Asn	Ser	Ser	Gln
	130					135					140				
Pro	Trp	Glu	Pro	Leu	Gln	Leu	His	Val	Asp	Lys	Ala	Val	Ser	Gly	Leu
145					150					155					160
Arg	Ser	Leu	Thr	Thr	Leu	Leu	Arg	Ala	Leu						

165

170

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

```

Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro
 1          5          10          15
Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr
          20          25          30
Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys
          35          40          45
Arg Thr Gly Asp Arg Gly Gly Gly Ser Ala Pro Pro Arg Leu Ile Cys
          50          55          60
Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu
65          70          75          80
Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu Asn Ile
          85          90          95
Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg Met Glu
          100          105          110
Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu Leu Ser
          115          120          125
Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser Gln Pro
          130          135          140
Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly Leu Arg
145          150          155          160
Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly
          165          170

```

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

```

Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu
 1          5          10          15
Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser
          20          25          30
Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg
          35          40          45
Thr Gly Asp Arg Gly Gly Gly Ser Ala Pro Pro Arg Leu Ile Cys Asp
          50          55          60
Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn
65          70          75          80
Ile Thr Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu Asn Ile Thr
          85          90          95
Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val
          100          105          110

```


Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu Leu Ser Glu
 115 120 125
 Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser Gln Pro Trp
 130 135 140
 Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly Leu Arg Ser
 145 150 155 160
 Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala
 165 170

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg
 1 5 10 15
 Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn
 20 25 30
 Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr
 35 40 45
 Gly Asp Arg Gly Gly Gly Ser Ala Pro Pro Arg Leu Ile Cys Asp Ser
 50 55 60
 Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile
 65 70 75 80
 Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val
 85 90 95
 Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly
 100 105 110
 Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala
 115 120 125
 Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser Gln Pro Trp Glu
 130 135 140
 Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly Leu Arg Ser Leu
 145 150 155 160
 Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln
 165 170

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr
 1 5 10 15
 Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe
 20 25 30
 Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly
 35 40 45
 Asp Arg Gly Gly Gly Ser Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg

50		55		60											
Val	Leu	Glu	Arg	Tyr	Leu	Glu	Ala	Lys	Glu	Ala	Glu	Asn	Ile	Thr	
65		70		75										80	
Thr	Gly	Cys	Ala	Glu	His	Cys	Ser	Leu	Asn	Glu	Asn	Ile	Thr	Val	Pro
		85		90										95	
Asp	Thr	Lys	Val	Asn	Phe	Tyr	Ala	Trp	Lys	Arg	Met	Glu	Val	Gly	Gln
		100		105										110	
Gln	Ala	Val	Glu	Val	Trp	Gln	Gly	Leu	Ala	Leu	Leu	Ser	Glu	Ala	Val
		115		120										125	
Leu	Arg	Gly	Gln	Ala	Leu	Leu	Val	Asn	Ser	Ser	Gln	Pro	Trp	Glu	Pro
		130		135										140	
Leu	Gln	Leu	His	Val	Asp	Lys	Ala	Val	Ser	Gly	Leu	Arg	Ser	Leu	Thr
145				150										155	160
Thr	Leu	Leu	Arg	Ala	Leu	Gly	Ala	Gln	Lys						
				165					170						

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Ala	Ile	Ser	Pro	Pro	Asp	Ala	Ala	Ser	Ala	Ala	Pro	Leu	Arg	Thr	Ile
1				5				10						15	
Thr	Ala	Asp	Thr	Phe	Arg	Lys	Leu	Phe	Arg	Val	Tyr	Ser	Asn	Phe	Leu
		20						25					30		
Arg	Gly	Lys	Leu	Lys	Leu	Tyr	Thr	Gly	Glu	Ala	Cys	Arg	Thr	Gly	Asp
		35					40					45			
Arg	Gly	Gly	Gly	Ser	Ala	Pro	Pro	Arg	Leu	Ile	Cys	Asp	Ser	Arg	Val
		50				55					60				
Leu	Glu	Arg	Tyr	Leu	Leu	Glu	Ala	Lys	Glu	Ala	Glu	Asn	Ile	Thr	Thr
65				70					75					80	
Gly	Cys	Ala	Glu	His	Cys	Ser	Leu	Asn	Glu	Asn	Ile	Thr	Val	Pro	Asp
			85					90						95	
Thr	Lys	Val	Asn	Phe	Tyr	Ala	Trp	Lys	Arg	Met	Glu	Val	Gly	Gln	Gln
		100					105						110		
Ala	Val	Glu	Val	Trp	Gln	Gly	Leu	Ala	Leu	Leu	Ser	Glu	Ala	Val	Leu
		115				120						125			
Arg	Gly	Gln	Ala	Leu	Leu	Val	Asn	Ser	Ser	Gln	Pro	Trp	Glu	Pro	Leu
		130				135					140				
Gln	Leu	His	Val	Asp	Lys	Ala	Val	Ser	Gly	Leu	Arg	Ser	Leu	Thr	Thr
145				150						155					160
Leu	Leu	Arg	Ala	Leu	Gly	Ala	Gln	Lys	Glu						
				165					170						

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

```

Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr
1      5      10      15
Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg
      20      25      30
Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp Arg
      35      40      45
Gly Gly Gly Ser Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu
      50      55      60
Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly
65      70      75      80
Cys Ala Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr
      85      90      95
Lys Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala
      100     105     110
Val Glu Val Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg
      115     120     125
Gly Gln Ala Leu Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln
      130     135     140
Leu His Val Asp Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu
145      150      155      160
Leu Arg Ala Leu Gly Ala Gln Lys Glu Ala
      165      170

```

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

```

Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala
1      5      10      15
Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly
      20      25      30
Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp Arg Gly
      35      40      45
Gly Gly Ser Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu
      50      55      60
Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys
65      70      75      80
Ala Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys
      85      90      95
Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val
      100     105     110
Glu Val Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly
      115     120     125
Gln Ala Leu Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu
      130     135     140
His Val Asp Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu
145      150      155      160
Arg Ala Leu Gly Ala Gln Lys Glu Ala Ile
      165      170

```

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

```

Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp
 1      5      10      15
Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys
      20      25      30
Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp Arg Gly Gly
      35      40      45
Gly Ser Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg
      50      55      60
Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala
65      70      75      80
Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val
      85      90      95
Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu
      100     105     110
Val Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln
      115     120     125
Ala Leu Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His
130     135     140
Val Asp Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg
145     150     155     160
Ala Leu Gly Ala Gln Lys Glu Ala Ile Ser
      165     170

```

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 170 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

```

Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr
 1      5      10      15
Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu
      20      25      30
Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp Arg Gly Gly Gly
      35      40      45
Ser Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr
      50      55      60
Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu
65      70      75      80
His Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn
      85      90      95
Phe Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val
      100     105     110
Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala
      115     120     125
Leu Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val
130     135     140
Asp Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala
145     150     155     160
Leu Gly Ala Gln Lys Glu Ala Ile Ser Pro

```

165

170

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

```

Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe
 1          5          10          15
Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys
          20          25          30
Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp Arg Gly Gly Gly Ser
          35          40          45
Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu
          50          55          60
Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His
65          70          75          80
Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe
          85          90          95
Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp
          100          105          110
Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu
          115          120          125
Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp
          130          135          140
Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu
145          150          155          160
Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro
          165          170

```

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

```

Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg
 1          5          10          15
Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu
          20          25          30
Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp Arg Gly Gly Gly Ser Ala
          35          40          45
Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu
          50          55          60
Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys
65          70          75          80
Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr
          85          90          95
Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln
100          105          110

```

```

Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu
   115               120               125
Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys
   130               135               140
Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly
  145               150               155               160
Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp
               165               170

```

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

```

Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys
  1               5               10               15
Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr
               20               25               30
Thr Gly Glu Ala Cys Arg Thr Gly Asp Arg Gly Gly Gly Ser Ala Pro
  35               40               45
Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu
  50               55               60
Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser
  65               70               75               80
Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala
               85               90               95
Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly
  100               105               110
Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val
  115               120               125
Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala
  130               135               140
Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala
  145               150               155               160
Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala
               165               170

```

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

```

Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu
  1               5               10               15
Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr
               20               25               30
Gly Glu Ala Cys Arg Thr Gly Asp Arg Gly Gly Gly Ser Ala Pro Pro
  35               40               45
Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala

```

50		55		60											
Lys	Glu	Ala	Glu	Asn	Ile	Thr	Thr	Gly	Cys	Ala	Glu	His	Cys	Ser	Leu
65				70						75					80
Asn	Glu	Asn	Ile	Thr	Val	Pro	Asp	Thr	Lys	Val	Asn	Phe	Tyr	Ala	Trp
			85						90					95	
Lys	Arg	Met	Glu	Val	Gly	Gln	Gln	Ala	Val	Glu	Val	Trp	Gln	Gly	Leu
			100					105					110		
Ala	Leu	Leu	Ser	Glu	Ala	Val	Leu	Arg	Gly	Gln	Ala	Leu	Leu	Val	Asn
		115					120					125			
Ser	Ser	Gln	Pro	Trp	Glu	Pro	Leu	Gln	Leu	His	Val	Asp	Lys	Ala	Val
		130				135					140				
Ser	Gly	Leu	Arg	Ser	Leu	Thr	Thr	Leu	Leu	Arg	Ala	Leu	Gly	Ala	Gln
145				150						155					160
Lys	Glu	Ala	Ile	Ser	Pro	Pro	Asp	Ala	Ala						
				165				170							

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Ala	Ala	Pro	Leu	Arg	Thr	Ile	Thr	Ala	Asp	Thr	Phe	Arg	Lys	Leu	Phe
1				5				10						15	
Arg	Val	Tyr	Ser	Asn	Phe	Leu	Arg	Gly	Lys	Leu	Lys	Leu	Tyr	Thr	Gly
		20						25					30		
Glu	Ala	Cys	Arg	Thr	Gly	Asp	Arg	Gly	Gly	Gly	Ser	Ala	Pro	Pro	Arg
		35				40					45				
Leu	Ile	Cys	Asp	Ser	Arg	Val	Leu	Glu	Arg	Tyr	Leu	Leu	Glu	Ala	Lys
		50			55					60					
Glu	Ala	Glu	Asn	Ile	Thr	Thr	Gly	Cys	Ala	Glu	His	Cys	Ser	Leu	Asn
65				70						75				80	
Glu	Asn	Ile	Thr	Val	Pro	Asp	Thr	Lys	Val	Asn	Phe	Tyr	Ala	Trp	Lys
			85					90						95	
Arg	Met	Glu	Val	Gly	Gln	Gln	Ala	Val	Glu	Val	Trp	Gln	Gly	Leu	Ala
			100				105						110		
Leu	Leu	Ser	Glu	Ala	Val	Leu	Arg	Gly	Gln	Ala	Leu	Leu	Val	Asn	Ser
		115				120					125				
Ser	Gln	Pro	Trp	Glu	Pro	Leu	Gln	Leu	His	Val	Asp	Lys	Ala	Val	Ser
		130			135					140					
Gly	Leu	Arg	Ser	Leu	Thr	Leu	Leu	Arg	Ala	Leu	Gly	Ala	Gln	Lys	
145				150				155						160	
Glu	Ala	Ile	Ser	Pro	Pro	Asp	Ala	Ala	Ser						
				165				170							

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

```

Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg
 1           5           10           15
Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu
           20           25           30
Ala Cys Arg Thr Gly Asp Arg Gly Gly Gly Ser Ala Pro Pro Arg Leu
           35           40           45
Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu
           50           55           60
Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu
65           70           75           80
Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg
           85           90           95
Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu
           100          105          110
Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser
           115          120          125
Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly
           130          135          140
Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu
145           150          155          160
Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala
           165          170

```

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

```

Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val
 1           5           10           15
Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala
           20           25           30
Cys Arg Thr Gly Asp Arg Gly Gly Gly Ser Ala Pro Pro Arg Leu Ile
           35           40           45
Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala
           50           55           60
Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu Asn
65           70           75           80
Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg Met
           85           90           95
Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu Leu
           100          105          110
Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser Gln
           115          120          125
Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly Leu
           130          135          140
Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu Ala
145           150          155          160
Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala
           165          170

```

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

```

Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr
 1           5           10           15
Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys
      20           25           30
Arg Thr Gly Asp Arg Gly Gly Gly Ser Ala Pro Pro Arg Leu Ile Cys
      35           40           45
Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu
      50           55           60
Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu Asn Ile
      65           70           75           80
Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg Met Glu
      85           90           95
Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu Leu Ser
      100           105           110
Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser Gln Pro
      115           120           125
Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly Leu Arg
      130           135           140
Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Ala Lys Glu Ala
      145           150           155           160
Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro
      165           170

```

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 170 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

```

Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser
 1           5           10           15
Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg
      20           25           30
Thr Gly Asp Arg Gly Gly Gly Ser Ala Pro Pro Arg Leu Ile Cys Asp
      35           40           45
Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn
      50           55           60
Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu Asn Ile Thr
      65           70           75           80
Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val
      85           90           95
Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu Leu Ser Glu
      100           105           110
Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser Gln Pro Trp
      115           120           125
Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly Leu Arg Ser
      130           135           140
Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu Ala Ile Ser
      145           150           155           160
Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu

```

165

170

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

```

Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn
 1             5             10             15
Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr
      20             25             30
Gly Asp Arg Gly Gly Gly Ser Ala Pro Pro Arg Leu Ile Cys Asp Ser
      35             40             45
Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile
      50             55             60
Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val
65             70             75             80
Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly
      85             90             95
Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala
      100            105            110
Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser Gln Pro Trp Glu
      115            120            125
Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly Leu Arg Ser Leu
      130            135            140
Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu Ala Ile Ser Pro
145            150            155            160
Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg
      165            170

```

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 512 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

```

AATATCACGA CGGGCTGTGC TGAACACTGC AGCTTGAATG AGAATATCAC TGTCCCAGAC      60
ACCAAAGTTA ATTTCTATGC CTGGAAGAGG ATGGAGGTCG GGCAGCAGGC CGTAGAAGTC      120
TGGCAGGGCC TGGCCCTGCT GTCGGAAGCT GTCCTGCGGG GCCAGGCCCT GTTGGTCAAC      180
TCTTCCCAGC CGTGGGAGCC CCTGCAGCTG CATGTGGATA AAGCCGTCAG TGGCCTTCGC      240
AGCCTCACCA CTCTGCTTCG GGCTCTGGGA GCCCAGAAGG AAGCCATCTC CCCTCCAGAT      300
GCGGCCTCAG CTGCTCCACT CCGAACAATC ACTGCTGACA CTTTCCGCAA ACTCTCCGA      360
GTCTACTCCA ATTTCTCCG GGGAAAGCTG AAGCTGTACA CAGGGGAGGC CTGCAGGACA      420
GGGACAGAT GAGGCGGCGG CTCCCCCAC CACGCCTCAT CTGTGACAGC CGAGTCTTGG      480
AGAGGTACCT CTTGGAGGCC AAGGAGGCCG AG                                512

```

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 512 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

ATCACGACGG	GCTGTGCTGA	ACACTGCAGC	TTGAATGAGA	ATATCACTGT	CCCAGACACC	60
AAAGTTAATT	TCTATGCCTG	GAAGAGGATG	GAGGTCGGGC	AGCAGGCCGT	AGAAGTCTGG	120
CAGGGCCTGG	CCCTGCTGTC	GGAAGCTGTC	CTGCGGGGCC	AGGCCCTGTT	GGTCAACTCT	180
TCCCAGCCGT	GGGAGCCCCT	GCAGCTGCAT	GTGGATAAAG	CCGTCAGTGG	CCTTCGCAGC	240
CTCACCACCTC	TGCTTCGGGC	TCTGGGAGCC	CAGAAGGAAG	CCATCTCCCC	TCCAGATGCG	300
GCCTCAGCTG	CTCCACTCCG	AACAATCACT	GCTGACACTT	TCCGCAAACCT	CTTCCGAGTC	360
TACTCCAATT	TCCTCCGGGG	AAAGCTGAAG	CTGTACACAG	GGGAGGCCTG	CAGGACAGGG	420
GACAGATGAG	GCGGCGGCTC	CCCCACCAC	GCCTCATCTG	TGACAGCCGA	GTCCTGGAGA	480
GGTACCTCTT	GGAGCCAAG	GAGGCCGAGA	AT			512

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 512 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

ACGACGGGCT	GTGCTGAACA	CTGCAGCTTG	AATGAGAATA	TCACTGTCCC	AGACACCAAA	60
GTTAATTTCT	ATGCCTGGAA	GAGGATGGAG	GTCGGGCAGC	AGGCCGTAGA	AGTCTGGCAG	120
GGCCTGGCCC	TGCTGTCGGA	AGCTGTCCTG	CGGGGCCAGG	CCCTGTTGGT	CAACTCTTCC	180
CAGCCGTGGG	AGCCCCTGCA	GCTGCATGTG	GATAAAGCCG	TCAGTGGCCT	TCGCAGCCTC	240
ACCACTCTGC	TTCGGGCTCT	GGGAGCCCAG	AAGGAAGCCA	TCTCCCCTCC	AGATGCGGCC	300
TCAGTCTGCT	CACCTCGAAC	AATCACTGCT	GACACTTTCC	GCAAACCTTT	CCGAGTCTAC	360
TCCAATTTCC	TCCGGGGAAA	GCTGAAGCTG	TACACAGGGG	AGGCCTGCAG	GACAGGGGAC	420
AGATGAGGCG	GCGGCTCCCC	CCACCACGCC	TCATCTGTGA	CAGCCGAGTC	CTGGAGAGGT	480
ACCTCTTGGA	GGCCAAGGAG	GCCGAGAATA	TC			512

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 512 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

ACGGGCTGTG	CTGAACACTG	CAGCTTGAAT	GAGAATATCA	CTGTCCCAGA	CACCAAAGTT	60
AATTTCTATG	CCTGGAAGAG	GATGGAGGTC	GGGCAGCAGG	CCGTAGAAGT	CTGGCAGGGC	120
CTGGCCCTGC	TGTCGGAAGC	TGTCCTGCGG	GGCCAGGCC	TGTTGGTCAA	CTCTTCCCAG	180
CCGTGGGAGC	CCCTGCAGCT	GCATGTGGAT	AAAGCCGTCA	GTGGCCTTCG	CAGCCTCACC	240
ACTCTGCTTC	GGGCTCTGGG	AGCCCAGAAG	GAAGCCATCT	CCCCTCCAGA	TGCGGCCTCA	300
GCTGCTCCAC	TCCGAACAAT	CACTGCTGAC	ACTTTCGCGA	AACTCTTCCG	AGTCTACTCC	360
AATTTCTCTC	GGGAAAAGCT	GAAGCTGTAC	ACAGGGGAGG	CCTGCAGGAC	AGGGGACAGA	420
TGAGGCGGCG	GCTCCCCCA	CCACGCCTCA	TCTGTGACAG	CCGAGTCCTG	GAGAGGTACC	480
TCTTGAGGC	CAAGGAGGCC	GAGAATATCA	CG			512

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 512 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

GGCTGTGCTG	AACACTGCAG	CTTGAATGAG	AATATCACTG	TCCCAGACAC	CAAAGTTAAT	60
TTCTATGCCT	GGAAGAGGAT	GGAGGTCGGG	CAGCAGGCCG	TAGAAGTCTG	GCAGGGCCTG	120
GCCCTGCTGT	CGGAAGCTGT	CCTGCGGGGC	CAGGCCCTGT	TGGTCAACTC	TTCCCAGCCG	180
TGGGAGCCCC	TGCAGCTGCA	TGTGGATAAA	GCCGTCAGTG	GCCTTCGCAG	CCTCACCCT	240
CTGCTTCGGG	CTCTGGGAGC	CCAGAAGGAA	GCCATCTCCC	CTCCAGATGC	GGCCTCAGCT	300
GCTCCTACTCC	GAACAATCAC	TGCTGACACT	TTCCGCAAAC	TCTTCCGAGT	CTACTCCAAT	360
TTCCTCCGGG	GAAAGCTGAA	GCTGTACACA	GGGGAGGCCT	GCAGGACAGG	GGACAGATGA	420
GGCGGGCGGCT	CCCCCACCA	CGCCTCATCT	GTGACAGCCG	AGTCCTGGAG	AGGTACCTCT	480
TGGAGGCCAA	GGAGGCCGAG	AATATCACGA	CG			512

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 512 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

TGTGCTGAAC	ACTGCAGCTT	GAATGAGAAT	ATCACTGTCC	CAGACACCAA	AGTTAATTTT	60
TATGCCTGGA	AGAGGATGGA	GGTCGGGCAG	CAGGCCGTAG	AAGTCTGGCA	GGGCCTGGCC	120
CTGCTGTCGG	AAGCTGTCCT	GCGGGGCCAG	GCCCTGTTGG	TCAACTCTTC	CCAGCCGTGG	180
GAGCCCCTGC	AGCTGCATGT	GGATAAAGCC	GTCAGTGGCC	TTGCGAGCCT	CACCACTCTG	240
CTTCGGGCTC	TGGGAGCCCA	GAAGGAAGCC	ATCTCCCCTC	CAGATGCGGC	CTCAGCTGCT	300
CCACTCCGAA	CAATCACTGC	TGACACTTTC	CGCAAACCTC	TCCGAGTCTA	CTCCAATTTT	360
CTCCGGGGAA	AGCTGAAGCT	GTACACAGGG	GAGGCCTGCA	GGACAGGGGA	CAGATGAGGC	420
GGCGGCTCCC	CCCACCACGC	CTCATCTGTG	ACAGCCGAGT	CCTGGAGAGG	TACCTCTTGG	480
AGGCCAAGGA	GGCCGAGAAT	ATCACGACGG	GC			512

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 512 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

GCTGAACACT	GCAGCTTGAA	TGAGAATATC	ACTGTCCCAG	ACACCAAAGT	TAATTTCTAT	60
GCCTGGAAGA	GGATGGAGGT	CGGGCAGCAG	GCCGTAGAAG	TCTGGCAGGG	CCTGGCCCTG	120
CTGTCGGAAG	CTGTCCTGCG	GGGCCAGGCC	CTGTTGGTCA	ACTCTTCCCA	GCCGTGGGAG	180
CCCCTGCAGC	TGCATGTGGA	TAAAGCCGTC	AGTGGCCTTC	GCAGCCTCAC	CACCTGTGCTT	240
CGGGCTCTGG	GAGCCCAGAA	GGAAGCCATC	TCCCCTCCAG	ATGCGGCCTC	AGCTGCTCCA	300
CTCCGAACAA	TCACTGCTGA	CACTTTCCGC	AAACTCTTCC	GAGTCTACTC	CAATTTCCCT	360
CGGGGAAAGC	TGAAGCTGTA	CACAGGGGAG	GCCTGCAAGG	CAGGGGACAG	ATGAGGCGGC	420
GGCTCCCCCC	ACCACGCCTC	ATCTGTGACA	GCCGAGTCCT	GGAGAGGTAC	CTCTTGAGAG	480
CCAAGGAGGC	CGAGAATATC	ACGACGGGCT	GT			512

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 512 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

GAACACTGCA	GCTTGAATGA	GAATATCACT	GTCCCAGACA	CCAAAGTTAA	TTTCTATGCC	60
TGGAAGAGGA	TGGAGGTCGG	GCAGCAGGCC	GTAAGAAGTCT	GGCAGGGCCT	GGCCCTGCTG	120
TCGGAAGCTG	TCCTGCGGGG	CCAGGCCCTG	TTGGTCAACT	CTTCCCAGCC	GTGGGAGCCC	180
CTGCAGCTGC	ATGTGGATAA	AGCCGTCAGT	GGCCTTCGCA	GCCTCACCAC	TCTGCTTCGG	240
GCTCTGGGAG	CCCAGAAGGA	AGCCATCTCC	CCTCCAGATG	CGGCCTCAGC	TGCTCCACTC	300
CGAAACAATCA	CTGCTGACAC	TTTCCGCAAA	CTCTTCCGAG	TCTACTCCAA	TTTCTCTCCG	360
GGAAAGCTGA	AGCTGTACAC	AGGGGAGGCC	TGCAGGACAG	GGGACAGATG	AGGCGGCGGC	420
TCCCCCACAC	ACGCCTCATC	TGTGACAGCC	GAGTCCTGGA	GAGGTACCTC	TTGGAGGCCA	480
AGGAGGCCGA	GAATATCACG	ACGGGCTGTG	CT			512

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 512 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

CACTGCAGCT	TGAATGAGAA	TATCACTGTC	CCAGACACCA	AAGTTAATTT	CTATGCCTGG	60
AAGAGGATGG	AGGTCGGGCA	GCAGGCCGTA	GAAGTCTGGC	AGGGCCTGGC	CCTGCTGTCG	120
GAAGCTGTCC	TGCGGGGCCA	GGCCCTGTG	GTCAACTCTT	CCCAGCCGTG	GGAGCCCCTG	180
CAGCTGCATG	TGGATAAAGC	CGTCAGTGCC	CTTCGCAGCC	TCACCACTCT	GCTTCGGGCT	240
CTGGGAGCCC	AGAAGGAAGC	CATCTCCCCT	CCAGATGCGG	CCTCAGCTGC	TCCACTCCGA	300
ACAATCACTG	CTGACACTTT	CCGCAAACTC	TTCCGAGTCT	ACTCCAATTT	CCTCCGGGGA	360
AAGCTGAAGC	TGTACACAGG	GGAGGCCTGC	AGGACAGGGG	ACAGATGAGG	CGGCGGCTCC	420
CCCCACCACG	CCTCATCTGT	GACAGCCGAG	TCCTGGAGAG	GTACCTCTTG	GAGGCCAAGG	480
AGGCCGAGAA	TATCACGACG	GGCTGTGCTG	AA			512

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 512 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

TGCAGCTTGA	ATGAGAATAT	CACTGTCCCA	GACACCAAAG	TTAATTTCTA	TGCCTGGAAG	60
AGGATGGAGG	TCGGGCAGCA	GGCCGTAGAA	GTCTGGCAGG	GCCTGGCCCT	GCTGTGCGAA	120
GCTGTCCTGC	GGGGCCAGGC	CCTGTTGGTC	AACTCTTCCC	AGCCGTGGGA	GCCCCGTCAG	180
CTGCATGTGG	ATAAAGCCGT	CAGTGGCCTT	CGCAGCCTCA	CCACTCTGCT	TCGGGCTCTG	240
GGAGCCCAGA	AGGAAGCCAT	CTCCCCCTCA	GATGCGGCCT	CAGCTGCTCC	ACTCCGAACA	300
ATCACTGCTG	ACACTTTCCG	CAAACCTCTC	CGAGTCTACT	CCAATTTCTT	CCGGGGAAAG	360
CTGAAGCTGT	ACACAGGGGA	GGCCTGCAGG	ACAGGGGACA	GATGAGGCGG	CGGCTCCCCC	420
CACCACGCCT	CATCTGTGAC	AGCCGAGTCC	TGGAGAGGTA	CCTCTTGAG	GCCAAGGAGG	480
CCGAGAATAT	CACGACGGGC	TGTGCTGAAC	AC			512

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 512 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

```

AGCTTGAATG AGAATATCAC TGTCCCAGAC ACCAAAGTTA ATTTCTATGC CTGGAAGAGG      60
ATGGAGGTCG GGCAGCAGGC CGTAGAAGTC TGGCAGGGCC TGGCCCTGCT GTCGGAAGCT      120
GTCCTGCGGG GCCAGGCCCT GTTGGTCAAC TCTTCCCAGC CGTGGGAGCC CTTGCAGCTG      180
CATGTGGATA AAGCCGTCAG TGGCCTTCGC AGCCTCACCA CTCTGCTTCG GGCTCTGGGA      240
GCCCAGAAGG AAGCCATCTC CCCTCCAGAT GCGGCCTCAG CTGCTCCACT CCGAACAATC      300
ACTGCTGACA CTTTCCGCAA ACTCTTCCGA GTCTACTCCA ATTTCTCCG GGGAAAGCTG      360
AAGCTGTACA CAGGGGAGGC CTGCAGGACA GGGGACAGAT GAGGCGGCGG CTCCCCCAGC      420
CACGCCTCAT CTGTGACAGC CGAGTCCTGG AGAGGTACCT CTTGGAGGCC AAGGAGGCCG      480
AGAATATCAC GACGGGCTGT GCTGAACACT GC                                     512

```

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 512 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

```

TTGAATGAGA ATATCACTGT CCCAGACACC AAAGTTAATT TCTATGCCTG GAAGAGGATG      60
GAGGTCGGGC AGCAGGCCGT AGAAGTCTGG CAGGGCCTGG CCCTGCTGTC GGAAGCTGTC      120
CTGCGGGGCC AGGCCCTGTT GGTCAACTCT TCCCAGCCGT GGGAGCCCCCT GCAGCTGCAT      180
GTGGATAAAG CCGTCAGTGG CTTTCGCAGC CTCACCACTC TGCTTCGGGC TCTGGGAGCC      240
CAGAAGGAAG CCATCTCCCC TCCAGATGCG GCCTCAGCTG CTCCACTCCG AACAACTACT      300
GCTGACACTT TCCGCAAACT CTTCCGAGTC TACTCCAATT TCCTCCGGGG AAAGCTGAAG      360
CTGTACACAG GGGAGGCTTG CAGGACAGGG GACAGATGAG GCGGCGGCTC CCCCCACCAC      420
GCCTCATCTG TGACAGCCGA GTCCTGGAGA GGTACCTCTT GGAGGCCAAG GAGGCCGAGA      480
ATATCACGAC GGGCTGTGCT GAACACTGCA GC                                     512

```

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 512 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

```

AATGAGAATA TCACTGTCCC AGACACCAA GTTAATTTCT ATGCCTGGAA GAGGATGGAG      60
GTCGGGCAGC AGGCCGTAGA AGTCTGGCAG GGCCTGGCCC TGCTGTCGGA AGCTGTCCTG      120
CGGGGCCAGG CCCTGTTGGT CAACTCTTCC CAGCCGTGGG AGCCCTGCA GCTGCATGTG      180
GATAAAGCCG TCAGTGGCCT TCGCAGCCTC ACCACTCTGC TTCGGGCTCT GGGAGCCCAG      240
AAGGAAGCCA TCTCCCTTCC AGATGCGGCC TCAGCTGCTC CACTCCGAAC AATCACTGCT      300
GACACTTTCC GCAAATCTT CCGAGTCTAC TCCAATTTCC TCCGGGGAAA GCTGAAGCTG      360
TACACAGGGG AGGCTTGAG GACAGGGGAG AGATGAGGCG GCGGCTCCCC CCACCACGCC      420
TCATCTGTGA CAGCCGAGTC CTGGAGAGGT ACCTCTTGGA GGCCAAGGAG GCCGAGAATA      480
TCACGACGGG CTGTGCTGAA CACTGCAGCT TG                                     512

```

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 512 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

GAGAATATCA	CTGTCCCAGA	CACCAAAGTT	AATTTCTATG	CCTGGAAGAG	GATGGAGGTC	60
GGGCAGCAGG	CCGTAGAAAGT	CTGGCAGGGC	CTGGCCCTGC	TGTCGGAAGC	TGTCCTGCGG	120
GGCCAGGCCC	TGTTGGTCAA	CTCTTCCCAG	CCGTGGGAGC	CCCTGCAGCT	GCATGTGGAT	180
AAAGCCGTCA	GTGGCCTTCG	CAGCCTCACC	ACTCTGCTTC	GGGCTCTGGG	AGCCCAGAAG	240
GAAGCCATCT	CCCCCTCCAGA	TGCGGCCCTCA	GCTGCTCCAC	TCCGAACAAT	CACTGCTGAC	300
ACTTTCCGCA	AACTCTTCCG	AGTCTACTCC	AATTTCTCTC	GGGAAAGCT	GAAGCTGTAC	360
ACAGGGGAGG	CCTGCAGGAC	AGGGGACAGA	TGAGGCGGCG	GCTCCCCCA	CCACGCCTCA	420
TCTGTGACAG	CCGAGTCCTG	GAGAGGTACC	TCTTGGAGGC	CAAGGAGGCC	GAGAATATCA	480
CGACGGGCTG	TGCTGAACAC	TGCAGCTTGA	AT			512

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 512 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

AATATCACTG	TCCCAGACAC	CAAAGTTAAT	TTCTATGCCT	GGAAGAGGAT	GGAGGTCGGG	60
CAGCAGGCCG	TAGAAGTCTG	GCAGGGCCTG	GCCCTGCTGT	CGGAAGCTGT	CCTGCGGGGC	120
CAGGCCCTGT	TGGTCAACTC	TTCCCAGCCG	TGGGAGCCCC	TGCAGCTGCA	TGTGGATAAA	180
GCCGTCACTG	GCCTTCGCAG	CCTCACCCT	CTGCTTCGGG	CTCTGGGAGC	CCAGAAGGAA	240
GCCATCTCCC	CTCCAGATGC	GGCCTCAGCT	GCTCCACTCC	GAACAATCAC	TGCTGACACT	300
TTCCGC AAAC	TCTTCCGAGT	CTACTCCAAT	TTCTTCCGGG	GAAAGCTGAA	GCTGTACACA	360
GGGGAGGCCT	GCAGGACAGG	GGACAGATGA	GGCGGCGGCT	CCCCCACCA	CGCCTCATCT	420
GTGACAGCCG	AGTCCTGGAG	AGGTACCTCT	TGGAGGCCAA	GGAGGCCGAG	AATATCACGA	480
CGGGCTGTGC	TGAACACTGC	AGCTTGAATG	AG			512

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 512 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

ATCACTGTCC	CAGACACCAA	AGTTAATTTT	TATGCCTGGA	AGAGGATGGA	GGTCGGGCAG	60
CAGGCCGTAG	AAGTCTGGCA	GGGCCTGGCC	CTGCTGTCTG	AAGCTGTCCT	GCGGGGCCAG	120
GCCCTGTTGG	TCAACTCTTC	CCAGCCGTGG	GAGCCCCTGC	AGCTGCATGT	GGATAAAGCC	180
GTCACTGGCC	TTTCGACGCT	CACCACTCTG	CTTCGGGCTC	TGGGAGCCCA	GAAGGAAGCC	240
ATCTCCCCCT	CAGATGCGGC	CTCAGCTGCT	CCACTCCGAA	CAATCACTGC	TGACACTTTC	300
CGCAAATCT	TCCGAGTCTA	CTCCAATTTT	CTCCGGGGAA	AGCTGAAGCT	GTACACAGGG	360
GAGCCCTGCA	GGACAGGGGA	CAGATGAGGC	GGCGGCTCCC	CCCACCACGC	CTCATCTGTG	420
ACAGCCGAGT	CCTGGAGAGG	TACCTCTTGG	AGGCCAAGGA	GGCCGAGAAT	ATCACGACGG	480
GCTGTGCTGA	ACACTGCAGC	TTGAATGAGA	AT			512

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

ACTGTCCCAG	ACACCAAAGT	TAATTTCTAT	GCCTGGAAGA	GGATGGAGGT	CGGGCAGCAG	60
GCCGTAGAAG	TCTGGCAGGG	CCTGGCCCTG	CTGTGCGAAG	CTGTCCTGCG	GGGCCAGGCC	120
CTGTTGGTCA	ACTCTTCCCA	GCCGTGGGAG	CCCCTGCAGC	TGCATGTGGA	TAAAGCCGTC	180
AGTGGCCTTC	GCAGCCTCAC	CACTCTGCTT	CGGGCTCTGG	GAGCCCAGAA	GGAAGCCATC	240
TCCCTCCAG	ATGCGGCCTC	AGCTGCTCCA	CTCCGAACAA	TCACTGCTGA	CACTTTCCGC	300
AAACTCTTCC	GAGTCTACTC	CAATTTCCCT	CGGGGAAAGC	TGAAGCTGTA	CACAGGGGAG	360
GCCTGCAGGA	CAGGGGACAG	ATGAGGCGGC	GGCTCCCCC	ACCACGCCTC	ATCTGTGACA	420
GCCGAGTCCT	GGAGAGGTAC	CTCTTGAGAG	CCAAGGAGGC	CGAGAATATC	ACGACGGGCT	480
GTGCTGAACA	CTGCAGCTTG	AATGAGAATA	ATC			513

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

GTCCCAGACA	CCAAAGTTAA	TTTCTATGCC	TGGAAGAGGA	TGGAGGTCGG	GCAGCAGGCC	60
GTAGAAGTCT	GGCAGGGCCT	GGCCCTGCTG	TCGGAAGCTG	TCCTGCGGGG	CCAGGCCCTG	120
TTGGTCAACT	CTTCCCAGCC	GTGGGAGCCC	CTGCAGCTGC	ATGTGGATAA	AGCCGTCAGT	180
GGCCTTCGCA	GCCTCACCAC	TCTGCTTCGG	GCTCTGGGAG	CCCAGAAGGA	AGCCATCTCC	240
CCTCCAGATG	CGGCCTCAGC	TGCTCCACTC	CGAACAATCA	CTGCTGACAC	TTTCCGCAAA	300
CTCTTCCGAG	TCTACTCCAA	TTTCCTCCGG	GGAAAGCTGA	AGCTGTACAC	AGGGGAGGCC	360
TGCAGGACAG	GGGACAGATG	AGGCGGCGGC	TCCCCCACC	ACGCCTCATC	TGTGACAGCC	420
GAGTCTTGGA	GAGGTACCTC	TTGGAGGCCA	AGGAGGCCGA	GAATATCACG	ACGGGCTGTG	480
CTGAACACTG	CAGCTTGAAT	GAGAATAATC	ACT			513

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

CCAGACACCA	AAGTTAATTT	CTATGCCTGG	AAGAGGATGG	AGGTGCGGCA	GCAGGCCGTA	60
GAAGTCTGGC	AGGGCCTGGC	CCTGCTGTGC	GAAGCTGTCC	TGCGGGGCCA	GGCCCTGTTG	120
GTCAACTCTT	CCCAGCCGTG	GGAGCCCCGT	CAGCTGCATG	TGGATAAAGC	CGTCAGTGGC	180
CTTCGCAGCC	TCACCACTCT	GCTTCGGGCT	CTGGGAGCCC	AGAAGGAAGC	CATCTCCCTT	240
CCAGATGCGG	CCTCAGCTGC	TCCACTCCGA	ACAATCACTG	CTGACACTTT	CCGCAAATCT	300
TTCCGAGTCT	ACTCCAATTT	CCTCCGGGGA	AAGCTGAAGC	TGTACACAGG	GGAGGCCTGC	360
AGGACAGGGG	ACAGATGAGG	CGGCGGCTCC	CCCCACCAG	CCTCATCTGT	GACAGCCGAG	420
TCCTGGAGAG	GTAGCTCTTG	GAGGCCAAGG	AGGCCGAGAA	TATCACGACG	GGCTGTGCTG	480
AACACTGCAG	CTTGAATGAG	AATAATCACT	GTC			513

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

GACACCAAAG	TTAATTCTA	TGCCTGGAAG	AGGATGGAGG	TCGGGCAGCA	GGCCGTAGAA	60
GTCTGGCAGG	GCCTGGCCCT	GCTGTCGGAA	GCTGTCCTGC	GGGGCCAGGC	CCTGTTGGTC	120
AACTCTTCCC	AGCCGTGGGA	GCCCCTGCA	CTGCATGTGG	ATAAAGCCGT	CAGTGGCCTT	180
CGCAGCCTCA	CCACTCTGCT	TCGGGCTCTG	GGAGCCCAGA	AGGAAGCCAT	CTCCCCCTCCA	240
GATGCGGCCT	CAGCTGCTCC	ACTCCGAACA	ATCACTGCTG	ACACTTTCCG	CAAACCTCTTC	300
CGAGTCTACT	CCAATTTCCT	CCGGGGAAAG	CTGAAGCTGT	ACACAGGGGA	GGCCTGCAGG	360
ACAGGGGACA	GATGAGGCGG	CGGCTCCCCC	CACCACGCCT	CATCTGTGAC	AGCCGAGTCC	420
TGGAGAGGTA	CCTCTTGGAG	GCCAAGGAGG	CCGAGAATAT	CACGACGGGC	TGTGCTGAAC	480
ACTGCAGCTT	GAATGAGAAT	AATCACTGTC	CCA			513

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

AGGATGGAGG	TCGGGCAGCA	GGCCGTAGAA	GTCTGGCAGG	GCCTGGCCCT	GCTGTCGGAA	60
GCTGTCCTGC	GGGGCCAGGC	CCTGTTGGTC	AACTCTTCCC	AGCCGTGGGA	GCCCCTGCA	120
CTGCATGTGG	ATAAAGCCGT	CAGTGGCCTT	CGCAGCCTCA	CCACTCTGCT	TCGGGCTCTG	180
GGAGCCCAGA	AGGAAGCCAT	CTCCCCCTCCA	GATGCGGCCT	CAGCTGCTCC	ACTCCGAACA	240
ATCACTGCTG	ACACTTTCCG	CAAACCTCTTC	CGAGTCTACT	CCAATTTCCT	CCGGGGAAAG	300
CTGAAGCTGT	ACACAGGGGA	GGCCTGCAGG	ACAGGGGACA	GATGAGGCGG	CGGCTCCCCC	360
CACCACGCCT	CATCTGTGAC	AGCCGAGTCC	TGGAGAGGTA	CCTCTTGGAG	GCCAAGGAGG	420
CCGAGAATAT	CACGACGGGC	TGTGCTGAAC	ACTGCAGCTT	GAATGAGAAT	AATCACTGTC	480
CCAGACACCA	AAGTTAATTT	CTATGCCTGG	AAG			513

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

ATGGAGGTCG	GGCAGCAGGC	CGTAGAAGTC	TGGCAGGGCC	TGGCCCTGCT	GTCGGAAGCT	60
GTCCTGCGGG	GCCAGGCCCT	GTTGGTCAAC	TCTTCCCAGC	CGTGGGAGCC	CCTGCAGCTG	120
CATGTGGATA	AAGCCGTCAG	TGGCCTTCGC	AGCCTCACCA	CTCTGCTTCG	GGCTCTGGGA	180
GCCCAGAAGG	AAGCCATCTC	CCCTCCAGAT	GCGGCCTCAG	CTGCTCCACT	CCGAACAATC	240
ACTGCTGACA	CTTTCGCAA	ACTCTTCCGA	GTCTACTCCA	ATTTCTCTCCG	GGGAAAGCTG	300
AAGCTGTACA	CAGGGGAGGC	CTGCAGGACA	GGGGACAGAT	GAGGCGGCGG	CTCCCCCAC	360
CACGCCTCAT	CTGTGACAGC	CGAGTCTTGG	AGAGGTACCT	CTTGGAGGCC	AAGGAGGCCG	420
AGAATATCAC	GACGGGCTGT	GCTGAACACT	GCAGCTTGAA	TGAGAATAAT	CACTGTCCCA	480
GACACCAAAG	TTAATTCTA	TGCCTGGAAG	AGG			513

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

GAGGTCGGGC	AGCAGGCCGT	AGAAGTCTGG	CAGGGCCTGG	CCCTGCTGTC	GGAAGCTGTC	60
CTGCGGGGCC	AGGCCCTGTT	GGTCAACTCT	TCCCAGCCGT	GGGAGCCCCT	GCAGCTGCAT	120
GTGGATAAAG	CCGTCAGTGG	CCTTCGCAGC	CTCACCCTC	TGCTTCGGGC	TCTGGGAGCC	180
CAGAAGGAAG	CCATCTCCCC	TCCAGATGCG	GCCTCAGCTG	CTCCACTCCG	AACAATCACT	240
GCTGACACTT	TCCGCAAACT	CTTCCGAGTC	TACTCCAATT	TCCTCCGGGG	AAAGCTGAAG	300
CTGTACACAG	GGGAGGCCTG	CAGGACAGGG	GACAGATGAG	GCGGCGGCTC	CCCCCACCAC	360
GCCTCATCTG	TGACAGCCGA	GTCTGGAGA	GGTACCTCTT	GGAGGCCAAG	GAGGCCGAGA	420
ATATCACGAC	GGGTGTGCT	GAACACTGCA	GCTTGAATGA	GAATAATCAC	TGTCCCAGAC	480
ACCAAAGTTA	ATTTCTATGC	CTGGAAGAGG	ATG			513

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

GTCGGGCAGC	AGGCCGTAGA	AGTCTGGCAG	GGCCTGGCCC	TGCTGTCGGA	AGCTGTCCTG	60
CGGGGCCAGG	CCCTGTTGGT	CAACTCTTCC	CAGCCGTGGG	AGCCCCCTGCA	GCTGCATGTG	120
GATAAAGCCG	TCAGTGGCCT	TCGCAGCCTC	ACCACTCTGC	TTCGGGCTCT	GGGAGCCAG	180
AAGGAAGCCA	TCCTCCCTCC	AGATGCGGCC	TCAGCTGCTC	CACTCCGAAC	AATCACTGCT	240
GACACTTTCC	GCAAACTCTT	CCGAGTCTAC	TCCAATTTCC	TCCGGGGAAA	GCTGAAGCTG	300
TACACAGGGG	AGGCCTGCAG	GACAGGGGAC	AGATGAGGCG	GCGGCTCCCC	CCACCACGCC	360
TCATCTGTGA	CAGCCGAGTC	CTGGAGAGGT	ACCTCTTGGA	GGCCAAGGAG	GCCGAGAATA	420
TCACGACGGG	CTGTGCTGAA	CACTGCAGCT	TGAATGAGAA	TAATCACTGT	CCCAGACACC	480
AAAGTTAATT	TCTATGCCTG	GAAGAGGATG	GAG			513

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

CAGGCCCTGT	TGGTCAACTC	TTCCCAGCCG	TGGGAGCCCC	TGCAGCTGCA	TGTGGATAAA	60
GCCGTCAGTG	GCCTTCGCAG	CCTCACCCT	CTGCTTCGGG	CTCTGGGAGC	CCAGAAGGAA	120
GCCATCTCCC	CTCCAGATGC	GGCCTCAGCT	GCTCCACTCC	GAACAATCAC	TGCTGACACT	180
TTCCGCAAAAC	TCCTCCGAGT	CTACTCCAAT	TTCTCCGGG	GAAAGCTGAA	GCTGTACACA	240
GGGGAGGCCT	GCAGGACAGG	GGACAGATGA	GGCGGCGGCT	CCCCCACCA	CGCCTCATCT	300
GTGACAGCCG	AGTCCTGGAG	AGGTACCTCT	TGGAGGCCAA	GGAGGCCGAG	AATATCACGA	360
CGGGCTGTGC	TGAACACTGC	AGCTTGAATG	AGAATAATCA	CTGTCCCAGA	CACCAAAGTT	420
AATTTCTATG	CCTGGAAGAG	GATGGAGGTC	GGGCAGCAGG	CCGTAGAAGT	CTGGCAGGGC	480
CTGGCCCTGC	TGTCGGAAGC	TGTCCTGCGG	GGC			513

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

GCCCTGTTGG	TCAACTCTTC	CCAGCCGTGG	GAGCCCCGTC	AGCTGCATGT	GGATAAAGCC	60
GTCAGTGGCC	TTCGCAGCCT	CACCACTCTG	CTTCGGGGCTC	TGGGAGCCCA	GAAGGAAGCC	120
ATCTCCCCTC	CAGATGCGGC	CTCAGCTGCT	CCACTCCGAA	CAATCACTGC	TGACACTTTC	180
CGCAAACCTC	TCCGAGTCTA	CTCCAATTTC	CTCCGGGGAA	AGCTGAAGCT	GTACACAGGG	240
GAGGCCTGCA	GGACAGGGGA	CAGATGAGGC	GGCGGCTCCC	CCCACCACGC	CTCATCTGTG	300
ACAGCCGAGT	CCTGGAGAGG	TACCTCTTGG	AGGCCAAGGA	GGCCGAGAAT	ATCACGACGG	360
GCTGTGCTGA	AACTGCGAGC	TTGAATGAGA	ATAATCACTG	TCCCAGACAC	CAAAGTTAAT	420
TTCTATGCCT	GGAAGAGGAT	GGAGGTCGGG	CAGCAGGCCG	TAGAAGTCTG	GCAGGGCCTG	480
GCCCTGCTGT	CGGAAGCTGT	CCTGCGGGGC	CAG			513

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

CTGTTGGTCA	ACTCTTCCCA	GCCGTGGGAG	CCCCTGCAGC	TGCATGTGGA	TAAAGCCGTC	60
AGTGGCCTTC	GCAGCCTCAC	CACTCTGCTT	CGGGCTCTGG	GAGCCCAGAA	GGAAGCCATC	120
TCCCCTCCAG	ATGCGGCCCTC	AGCTGCTCCA	CTCCGAACAA	TCACTGCTGA	CACTTTCCGC	180
AAACTCTTCC	GAGTCTACTC	CAATTTCTCT	CGGGGAAAGC	TGAAGCTGTA	CACAGGGGAG	240
GCCTGCAGGA	CAGGGGACAG	ATGAGGCGGC	GGCTCCCCCT	ACCACGCCTC	ATCTGTGACA	300
GCCGAGTCCT	GGAGAGGTAC	CTCTTGGAGG	CCAAGGAGGC	CGAGAATATC	ACGACGGGCT	360
GTGCTGAACA	CTGCAGCTTG	AATGAGAATA	ATCACTGTCC	CAGACACCAA	AGTTAATTTT	420
TATGCCTGGA	AGAGGATGGA	GGTCGGGCAG	CAGGCCGTAG	AAGTCTGGCA	GGGCCTGGCC	480
CTGCTGTCGG	AAGCTGTCCT	GCGGGGCCAG	GCC			513

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

TTGGTCAACT	CTTCCCAGCC	GTGGGAGCCC	CTGCAGCTGC	ATGTGGATAA	AGCCGTCAGT	60
GGCCTTCGCA	GCCTCACAC	TCTGCTTCGG	GCTCTGGGAG	CCCAGAAGGA	AGCCATCTCC	120
CCTCCAGATG	CGGCCTCAGC	TGCTCCACTC	CGAACAATCA	CTGCTGACAC	TTTCCGCAAA	180
CTCTTCCGAG	TCTACTCCAA	TTTCTTCCGG	GGAAAGCTGA	AGCTGTACAC	AGGGGAGGCC	240
TGCAGGACAG	GGGACAGATG	AGGCGGCGGC	TCCCCCACC	ACGCCTCATC	TGTGACAGCC	300
GAGTCCTGGA	GAGGTACCTC	TTGGAGGCCA	AGGAGGCCGA	GAATATCACG	ACGGGCTGTG	360
CTGAACACTG	CAGCTTGAAT	GAGAATAATC	ACTGTCCCAG	ACACCAAAGT	TAATTTCTAT	420
GCCTGGAAGA	GGATGGAGGT	CGGGCAGCAG	GCCGTAGAAG	TCTGGCAGGG	CCTGGCCCTG	480
CTGTGGAAG	CTGTCCTGCG	GGGCCAGGCC	CTG			513

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

GTCAACTCTT	CCCAGCCGTG	GGAGCCCCTG	CAGCTGCATG	TGGATAAAGC	CGTCAGTGGC	60
CTTCGCAGCC	TCACCACTCT	GCTTCGGGCT	CTGGGAGCCC	AGAAGGAAGC	CATCTCCCCT	120
CCAGATGCGG	CCTCAGCTGC	TCCACTCCGA	ACAATCACTG	CTGACACTTT	CCGCAAACCTC	180
TTCCGAGTCT	ACTCCAATTT	CCTCCGGGGA	AAGCTGAAGC	TGTACACAGG	GGAGGCCTGC	240
AGGACAGGGG	ACAGATGAGG	CGGCGGCTCC	CCCCACCACG	CCTCATCTGT	GACAGCCGAG	300
TCCTGGAGAG	GTACCTCTTG	GAGGCCAAGG	AGGCCGAGAA	TATCACGACG	GGCTGTGCTG	360
AACACTGCAG	CTTGAATGAG	AATAATCACT	GTCCCAGACA	CCAAAGTTAA	TTTCTATGCC	420
TGGAAGAGGA	TGGAGGTCGG	GCAGCAGGCC	GTAGAAGTCT	GGCAGGGCCT	GGCCCTGCTG	480
TCGGAAGCTG	TCCTGCGGGG	CCAGGCCCTG	TTG			513

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

AACTCTTCCC	AGCCGTGGGA	GGCCCTGCAG	CTGCATGTGG	ATAAAGCCGT	CAGTGGCCTT	60
CGCAGCCTCA	CCACTCTGCT	TCGGGCTCTG	GGAGCCCAGA	AGGAAGCCAT	CTCCCCTCCA	120
GATGCGGCCT	CAGCTGCTCC	ACTCCGAACA	ATCACTGCTG	ACACTTTCCG	CAAACCTCTC	180
CGAGTCTACT	CCAATTTCCCT	CCGGGGAAAG	CTGAAGCTGT	ACACAGGGGA	GGCCTGCAGG	240
ACAGGGGACA	GATGAGGCGG	CGGCTCCCCC	CACCACGCCT	CATCTGTGAC	AGCCGAGTCC	300
TGGAGAGGTA	CCTCTTGGAG	GCCAAGGAGG	CCGAGAATAT	CACGACGGGC	TGTGCTGAAC	360
ACTGCAGCTT	GAATGAGAAT	AATCACTGTC	CCAGACACCA	AAGTTAATTT	CTATGCCTGG	420
AAGAGGATGG	AGGTCGGGCA	GCAGGCCGTA	GAAGTCTGGC	AGGGCCTGGC	CCTGCTGTGC	480
GAAGCTGTCC	TGCGGGGCCA	GGCCCTGTTG	GTC			513

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

TCTTCCCAGC	CGTGGGAGCC	CCTGCAGCTG	CATGTGGATA	AAGCCGTCAG	TGGCCTTCGC	60
AGCCTCACCA	CTCTGCTTCG	GGCTCTGGGA	GCCCAGAAGG	AAGCCATCTC	CCCTCCAGAT	120
GCGGCCTCAG	CTGCTCCACT	CCGAACAATC	ACTGCTGACA	CTTTCCGCAA	ACTCTTCCGA	180
GTCTACTCCA	ATTTCTCCCG	GGGAAAGCTG	AAGCTGTACA	CAGGGGAGGC	CTGCAGGACA	240
GGGGACAGAT	GAGGCGGCGG	CTCCCCCAC	CACGCCTCAT	CTGTGACAGC	CGAGTCTTGG	300
AGAGGTACCT	CTTGGAGGCC	AAGGAGGCCG	AGAATATCAC	GACGGGCTGT	GCTGAACACT	360
GCAGCTTGAA	TGAGAATAAT	CACTGTCCCA	GACACCAAAG	TTAATTTCTA	TGCCTGGAAG	420
AGGATGGAGG	TCGGGCAGCA	GGCCGTAGAA	GTCTGGCAGG	GCCTGGCCCT	GCTGTCCGAA	480
GCTGTCTTGC	GGGGCCAGGC	CCTGTTGGTC	AAC			513

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

TCCCAGCCGT	GGGAGCCCT	GCAGCTGCAT	GTGGATAAAG	CCGTCAGTGG	CCTTCGCAGC	60
CTCACCCTC	TGCTTCGGG	TCTGGGAGCC	CAGAAGGAAG	CCATCTCCCC	TCCAGATGCG	120
GCCTCAGCTG	CTCCACTCCG	AACAATCACT	GCTGACACTT	TCCGCAAACT	CTTCCGAGTC	180
TACTCCAATT	TCCTCCGGGG	AAAGCTGAAG	CTGTACACAG	GGGAGGCCTG	CAGGACAGGG	240
GACAGATGAG	GCGGCGGCTC	CCCCACCAC	GCCTCATCTG	TGACAGCCGA	GTCCCTGGAGA	300
GGTACCTCTT	GGAGGCCAAG	GAGGCCGAGA	ATATCACGAC	GGGCTGTGCT	GAACACTGCA	360
GCTTGAATGA	GAATAATCAC	TGTCCCAGAC	ACCAAAGTTA	ATTCTATATG	CTGGAAGAGG	420
ATGGAGGTCG	GGCAGCAGGC	CGTAGAAGTC	TGGCAGGGCC	TGGCCCTGCT	GTCGGAAGCT	480
GTCTGCGGG	GCCAGGCCCT	GTTGGTCAAC	TCT			513

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

CAGCCGTGGG	AGCCCCCTGCA	GCTGCATGTG	GATAAAGCCG	TCAGTGGCCT	TCGCAGCCTC	60
ACCACTCTGC	TTCGGGCTCT	GGGAGCCCAG	AAGGAAGCCA	TCTCCCTCC	AGATGCGGCC	120
TCAGCTGCTC	CACTCCGAAC	AATCACTGCT	GACACTTTCC	GCAAACCTCT	CCGAGTCTAC	180
TCCAATTTCC	TCCGGGGAAA	GCTGAAGCTG	TACACAGGGG	AGGCCTGCAG	GACAGGGGAC	240
AGATGAGGCG	GCGGCTCCCC	CCACCACGCC	TCATCTGTGA	CAGCCGAGTC	CTGGAGAGGT	300
ACCTCTTGGA	GGCCAAGGAG	GCCGAGAATA	TCACGACGGG	CTGTGCTGAA	CACTGCAGCT	360
TGAATGAGAA	TAATCACTGT	CCAGACACC	AAAGTTAATT	TCTATGCCTG	GAAGAGGATG	420
GAGGTCGGGC	AGCAGGCCGT	AGAAGTCTGG	CAGGGCCTGG	CCCTGCTGTC	GGAAGCTGTC	480
CTGCGGGGCC	AGGCCCTGTT	GGTCAACTCT	TCC			513

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

CCGTGGGAGC	CCCTGCAGCT	GCATGTGGAT	AAAGCCGTCA	GTGGCCTTCG	CAGCCTCACC	60
ACTCTGCTTC	GGGCTCTGGG	AGCCCAGAAG	GAAGCCATCT	CCCCCTCAGA	TGCGGCCCTCA	120
GCTGCTCCAC	TCCGAACAAT	CACTGCTGAC	ACTTTCCGCA	AACTCTTCCG	AGTCTACTCC	180
AATTTCCTCC	GGGGAAAGCT	GAAGCTGTAC	ACAGGGGAGG	CCTGCAGGAC	AGGGGACAGA	240
TGAGCGGCG	GCTCCCCCA	CCACGCCTCA	TCTGTGACAG	CCGAGTCCTG	GAGAGGTACC	300
TCTTGAGGC	CAAGGAGGCC	GAGAATATCA	CGACGGGCTG	TGCTGAACAC	TGCAGCTTGA	360
ATGAGAATAA	TCAGTGTCCT	AGACACCAA	GTTAATTTCT	ATGCCTGGAA	GAGGATGGAG	420
GTCCGGCAGC	AGGCCGTAGA	AGTCTGGCAG	GGCCTGGCCC	TGCTGTCCGA	AGCTGTCTCT	480
CGGGGCCAGG	CCCTGTTGGT	CAACTCTTCC	CAG			513

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

TGGGAGCCCC	TGCAGCTGCA	TGTGGATAAA	GCCGTCAGTG	GCCTTCGCAG	CCTCACCCT	60
CTGCTTCGGG	CTCTGGGAGC	CCAGAAGGAA	GCCATCTCCC	CTCCAGATGC	GGCCTCAGCT	120
GCTCCACTCC	GAACAATCAC	TGCTGACACT	TTCCGCAAAC	TCTTCCGAGT	CTACTCCAAT	180
TTCTCCGGG	GAAAGCTGAA	GCTGTACACA	GGGGAGGCCT	GCAGGACAGG	GGACAGATGA	240
GGCGGCGGCT	CCCCCACCAC	CGCCTCATCT	GTGACAGCCG	AGTCCTGGAG	AGGTACCTCT	300
TGGAGGCCAA	GGAGGCCGAG	AATATCACGA	CGGGCTGTGC	TGAACACTGC	AGCTTGAATG	360
AGAATAATCA	CTGTCCCAGA	CACCAAAGTT	AATTTCTATG	CCTGGAAGAG	GATGGAGGTC	420
GGGACAGCAG	CCGTAGAAAGT	CTGGCAGGGC	CTGGCCCTGC	TGTCGGAAGC	TGTCCTGCGG	480
GGCCAGGCC	TGTTGGTCAA	CTCTTCCCAG	CCG			513

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

GAGCCCCTGC	AGCTGCATGT	GGATAAAGCC	GTCAGTGGCC	TTCGCAGCCT	CACCACTCTG	60
CTTCGGGCTC	TGGGAGCCCA	GAAGGAAGCC	ATCTCCCCTC	CAGATGCGGC	CTCAGCTGCT	120
CCACTCCGAA	CAATCACTGC	TGACACTTTC	CGCAAACCTC	TCCGAGTCTA	CTCCAATTTT	180
CTCCGGGGAA	AGCTGAAGCT	GTACACAGGG	GAGGCCTGCA	GGACAGGGGA	CAGATGAGGC	240
GGCGGCTCCC	CCCACCACGC	CTCATCTGTG	ACAGCCGAGT	CCTGGAGAGG	TACCTCTTGG	300
AGGCCAAGGA	GGCCGAGAAT	ATCACGACGG	GCTGTGCTGA	ACACTGCAGC	TTGAATGAGA	360
ATAATCACTG	TCCCAGACAC	CAAAGTTAAT	TTCTATGCCT	GGAAGAGGAT	GGAGGTCGGG	420
CAGCAGGCCG	TAGAAGTCTG	GCAGGGCCTG	GCCCTGCTGT	CGGAAGCTGT	CCTGCGGGGC	480
CAGGCCCTGT	TGGTCAACTC	TTCCCAGCCG	TGG			513

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

CTTCGGGCTC	TGGGAGCCCA	GAAGGAAGCC	ATCTCCCCTC	CAGATGCGGC	CTCAGCTGCT	60
CCACTCCGAA	CAATCACTGC	TGACACTTTC	CGCAAACCTC	TCCGAGTCTA	CTCCAATTTT	120
CTCCGGGGAA	AGCTGAAGCT	GTACACAGGG	GAGGCCTGCA	GGACAGGGGA	CAGATGAGGC	180
GGCGGCTCCC	CCCACCACGC	CTCATCTGTG	ACAGCCGAGT	CCTGGAGAGG	TACCTCTTGG	240
AGGCCAAGGA	GGCCGAGAAT	ATCACGACGG	GCTGTGCTGA	ACACTGCAGC	TTGAATGAGA	300
ATAATCACTG	TCCCAGACAC	CAAAGTTAAT	TTCTATGCCT	GGAAGAGGAT	GGAGGTCGGG	360
CAGCAGGCCG	TAGAAGTCTG	GCAGGGCCTG	GCCCTGCTGT	CGGAAGCTGT	CCTGCGGGGC	420
CAGGCCCTGT	TGGTCAACTC	TTCCCAGCCG	TGGGAGCCCC	TGCAGCTGCA	TGTGGATAAA	480
GCCGTCAGTG	GCCTTCGCAG	CCTCACCCT	CTG			513

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

CGGGCTCTGG	GAGCCAGAA	GGAAGCCATC	TCCCCTCCAG	ATGCGGCCTC	AGCTGCTCCA	60
CTCCGAACAA	TCACTGCTGA	CACTTTCGCG	AAACTCTTCC	GAGTCTACTC	CAATTTCCTC	120
CGGGGAAAGC	TGAAGCTGTA	CACAGGGGAG	GCCTGCAGGA	CAGGGGACAG	ATGAGGCGGC	180
GGCTCCCCC	ACCACGCCTC	ATCTGTGACA	GCCGAGTCCT	GGAGAGGTAC	CTCTTGGAGG	240
CCAAGGAGGC	CGAGAATATC	ACGACGGGCT	GTGCTGAACA	CTGCAGCTTG	AATGAGAATA	300
ATCACTGTCC	CAGACACCAA	AGTTAATTTC	TATGCCTGGA	AGAGGATGGA	GGTCGGGCAG	360
CAGGCCGTAG	AAGTCTGGCA	GGGCCTGGCC	CTGCTGTCGG	AAGCTGTCCT	GCGGGGCCAG	420
GCCCTGTTGG	TCAACTCTTC	CCAGCCGTGG	GAGCCCCTGC	AGCTGCATGT	GGATAAAGCC	480
GTCAGTGGCC	TTGCAGCCT	CACCACTCTG	CTT			513

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

GCTCTGGGAG	CCCAGAAGGA	AGCCATCTCC	CCTCCAGATG	CGGCCTCAGC	TGCTCCACTC	60
CGAACAAATCA	CTGCTGACAC	TTTCCGCAAA	CTCTTCCGAG	TCTACTCCAA	TTTCCTCCGG	120
GGAAAGCTGA	AGCTGTACAC	AGGGGAGGCC	TGCAGGACAG	GGGACAGATG	AGGCGGCGGC	180
TCCCCCACC	ACGCCTCATC	TGTGACAGCC	GAGTCCTGGA	GAGGTACCTC	TTGGAGGCCA	240
AGGAGGCCGA	GAATATCACG	ACGGGCTGTG	CTGAACACTG	CAGCTTGAAT	GAGAATAATC	300
ACTGTCCCAG	ACACCAAAGT	TAATTTCTAT	GCCTGGAAGA	GGATGGAGGT	CGGGCAGCAG	360
GCCGTAGAAG	CTTGGCAGGG	CCTGGCCCTG	CTGTCGGAAG	CTGTCCTGCG	GGGCCAGGCC	420
CTGTTGGTCA	ACTCTTCCCA	GCCGTGGGAG	CCCCTGCAGC	TGCATGTGGA	TAAAGCCGTC	480
AGTGGCCTTC	GCAGCCTCAC	CACTCTGCTT	CGG			513

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

CTGGGAGCCC	AGAAGGAAGC	CATCTCCCTT	CCAGATGCGG	CCTCAGCTGC	TCCACTCCGA	60
ACAATCACTG	CTGACACTTT	CCGCAAATC	TTCCGAGTCT	ACTCCAATTT	CCTCCGGGGA	120
AAGCTGAAGC	TGTACACAGG	GGAGGCCTGC	AGGACAGGGG	ACAGATGAGG	CGGCGGCTCC	180
CCCCACCACG	CCTCATCTGT	GACAGCCGAG	TCCTGGAGAG	GTACCTCTTG	GAGGCCAAGG	240
AGGCCGAGAA	TATCACGACG	GGCTGTGCTG	AACACTGCAG	CTTGAATGAG	AATAATCACT	300
GTCCAGACA	CCAAAGTTAA	TTTCTATGCC	TGGAAGAGGA	TGGAGGTCGG	GCAGCAGGCC	360
GTAGAAGTCT	GGCAGGGCCT	GGCCCTGCTG	TCGGAAGCTG	TCCTGCGGGG	CCAGGCCCTG	420
TTGGTCAACT	CTTCCAGGCC	GTGGGAGCCC	CTGCAGCTGC	ATGTGGATAA	AGCCGTCAGT	480
GCCTTCGCA	GCCTCACCAC	TCTGCTTCGG	GTC			513

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

GGAGCCCAGA	AGGAAGCCAT	CTCCCCCTCCA	GATGCGGCCT	CAGCTGCTCC	ACTCCGAACA	60
ATCACTGCTG	ACACTTTCCG	CAAACCTCTC	CGAGTCTACT	CCAATTTCCCT	CCGGGGAAAAG	120
CTGAAGCTGT	ACACAGGGGA	GGCCTGCAGG	ACAGGGGACA	GATGAGGCGG	CGGCTCCCCC	180
CACCACGCCT	CATCTGTGAC	AGCCGAGTCC	TGGAGAGGTA	CCTCTTGGAG	GCCAAGGAGG	240
CCGAGAATAT	CACGACGGGC	TGTGCTGAAC	ACTGCAGCTT	GAATGAGAAT	AATCACTGTC	300
CCAGACACCA	AAGTTAATTT	CTATGCCTGG	AAGAGGATGG	AGGTCGGGCA	GCAGGCCGTA	360
GAAGTCTGGC	AGGGCCTGGC	CCTGCTGTGC	GAAGCTGTCC	TGCGGGGCCA	GGCCCTGTTG	420
GTCAACTCTT	CCGACCCGTG	GGAGCCCCTG	CAGCTGCATG	TGGATAAAGC	CGTCAGTGCC	480
CTTCGCAGCC	TCACCACTCT	GCTTCGGGCT	CTG			513

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 513 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

GCCCAGAAGG	AAGCCATCTC	CCCTCCAGAT	GCGGCCTCAG	CTGCTCCACT	CCGAACAATC	60
ACTGCTGACA	CTTTCCGCAA	ACTCTTCCGA	GTCTACTCCA	ATTTCTCTCCG	GGGAAAGCTG	120
AAGCTGTACA	CAGGGGAGGC	CTGCAGGACA	GGGGACAGAT	GAGGCGGCGG	CTCCCCCCAC	180
CACGCCTCAT	CTGTGACAGC	CGAGTCCTGG	AGAGGTACCT	CTTGGAGGCC	AAGGAGGCCG	240
AGAATATCAC	GACGGGCTGT	GCTGAACACT	GCAGCTTGAA	TGAGAATAAT	CACTGTCCCCA	300
GACACCAAAG	TTAATTTCTA	TGCCCTGGAAG	AGGATGGAGG	TCGGGCAGCA	GGCCGTAGAA	360
GTCTGGCAGG	GCCTGGCCCT	GCTGTCGGAA	GCTGTCTGTC	GGGGCCAGGC	CCTGTTGGTC	420
AACTCTTCCC	AGCCGTGGGA	GCCCCGTGAG	CTGCATGTGG	ATAAAGCCGT	CAGTGGCCTT	480
CGCAGCCTCA	CCACTCTGCT	TCGGGCTCTG	GGA			513

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 513 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

CAGAAGGAAG	CCATCTCCCC	TCCAGATGCG	GCCTCAGCTG	CTCCACTCCG	AACAATCACT	60
GCTGACACTT	TCCGCAAAC	CTTCCGAGTC	TACTCCAATT	TCCTCCGGGG	AAAGCTGAAG	120
CTGTACACAG	GGGAGGCCTG	CAGGACAGGG	GACAGATGAG	GCGGCGGCTC	CCCCCACCAC	180
GCCTCATCTG	TGACAGCCGA	GTCTTGGAGA	GGTACCTCTT	GGAGGCCAAG	GAGGCCGAGA	240
ATATCACGAC	GGGCTGTGCT	GAACACTGCA	GCTTGAATGA	GAATAATCAC	TGTCCAGAC	300
ACCAAAGTTA	ATTTCTATGC	CTGGAAGAGG	ATGGAGGTCG	GGCAGCAGGC	CGTAGAAGTC	360
TGGCAGGGCC	TGGCCCTGCT	GTGGAAGCT	GTCTGCGGG	GCCAGGCCCT	GTTGGTCAAC	420
TCTTCCCAGC	CGTGGGAGCC	CCTGCAGCTG	CATGTGGATA	AAGCCGTCAG	TGGCCTTCGC	480
AGCCTCACCA	CTCTGCTTCG	GGCTCTGGGA	GCC			513

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 513 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

AAGGAAGCCA	TCTCCCCTCC	AGATGCGGCC	TCAGCTGCTC	CACTCCGAAC	AATCACTGCT	60
GACACTTTCC	GCAAACCTCT	CCGAGTCTAC	TCCAATTTCC	TCCGGGGAAA	GCTGAAGCTG	120
TACACAGGGG	AGGCCCTGCAG	GACAGGGGAC	AGATGAGGCG	GCGGCTCCCC	CCACCACGCC	180
TCATCTGTGA	CAGCCGAGTC	CTGGAGAGGT	ACCTCTTGGA	GGCCAAGGAG	GCCGAGAATA	240
TCACGACGGG	CTGTGCTGAA	CACTGCAGCT	TGAATGAGAA	TAATCACTGT	CCCAGACACC	300
AAAGTTAATT	TCTATGCCTG	GAAGAGGATG	GAGGTCGGGC	AGCAGGCCGT	AGAAGTCTGG	360
CAGGGCCTGG	CCCTGCTGTC	GGAAGCTGTC	CTGCGGGGCC	AGGCCCTGTT	GGTCAACTCT	420
TCCCAGCCGT	GGGAGCCCCT	GCAGCTGCAT	GTGGATAAAG	CCGTCAGTGG	CCTTCGCAGC	480
CTCACCCTC	TGCTTCGGGC	TCTGGGAGCC	CAG			513

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

GAAGCCATCT	CCCCTCCAGA	TGCGGCCTCA	GCTGCTCCAC	TCCGAACAAT	CACTGCTGAC	60
ACTTTCCGCA	AACTCTTCCG	AGTCTACTCC	AATTTCTCTC	GGGGAAGCT	GAAGCTGTAC	120
ACAGGGGAGG	CTTGCAGGAC	AGGGGACAGA	TGAGGCGGCG	GCTCCCCCA	CCACGCCTCA	180
TCTGTGACAG	CCGAGTCCCTG	GAGAGGTACC	TCTTGAGGCG	CAAGGAGGCC	GAGAATATCA	240
CGACGGGCTG	TGCTGAACAC	TGCAGCTTGA	ATGAGAATAA	TCACTGTCCC	AGACACCAAA	300
GTTAATTTCT	ATGCCTGGAA	GAGGATGGAG	GTCGGGCAGC	AGGCCGTAGA	AGTCTGGCAG	360
GGCCTGGCCC	TGCTGTCGGA	AGCTGTCCTG	CGGGGCCAGG	CCCTGTTGGT	CAACTCTTCC	420
CAGCCGTGGG	AGCCCCTGCA	GCTGCATGTG	GATAAAGCCG	TCAGTGGCCT	TCGCAGCCTC	480
ACCACTCTGC	TTGGGCTCT	GGGAGCCCAG	AAG			513

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

GCCATCTCCC	CTCCAGATGC	GGCCTCAGCT	GCTCCACTCC	GAACAATCAC	TGCTGACACT	60
TTCCGCAAAC	TCTTCCGAGT	CTACTCCAAT	TTCTTCCGGG	GAAAGCTGAA	GCTGTACACA	120
GGGGAGGCCT	GCAGGACAGG	GGACAGATGA	GGCGGCGGCT	CCCCCACCA	CGCCTCATCT	180
GTGACAGCCG	AGTCCTGGAG	AGGTACCTCT	TGGAGGCCAA	GGAGGCCGAG	AATATCACGA	240
CGGGCTGTGC	TGAACACTGC	AGCTTGAATG	AGAATAATCA	CTGTCCCAGA	CACCAAAGTT	300
AATTTCTATG	CCTGGAAGAG	GATGGAGGTC	GGGCAGCAGG	CCGTAGAAGT	CTGGCAGGGC	360
CTGGCCCTGC	TGTCGGAAGC	TGTCCTGCGG	GGCCAGGCC	TGTTGGTCAA	CTCTTCCCAG	420
CCGTGGGAGC	CCCTGCAGCT	GCATGTGGAT	AAAGCCGTCA	GTGGCCTTCG	CAGCCTCACC	480
ACTCTGCTTC	GGGCTCTGGG	AGCCCAGAAG	GAA			513

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

ATCTCCCCTC	CAGATGCGGC	CTCAGCTGCT	CCACTCCGAA	CAATCACTGC	TGACACTTTC	60
CGCAAACCTCT	TCCGAGTCTA	CTCCAATTTC	CTCCGGGGAA	AGCTGAAGCT	GTACACAGGG	120
GAGGCCTGCA	GGACAGGGGA	CAGATGAGGC	GGCGGCTCCC	CCCACCACGC	CTCATCTGTG	180
ACAGCCGAGT	CCTGGAGAGG	TACCTCTTGG	AGGCCAAGGA	GGCCGAGAAT	ATCACGACGG	240
GCTGTGCTGA	ACACTGCAGC	TTGAATGAGA	ATAATCACTG	TCCCAGACAC	CAAAGTTAAT	300
TTCTATGCCT	GGAAGAGGAT	GGAGGTCGGG	CAGCAGGCCG	TAGAAGTCTG	GCAGGCCTG	360
GCCCTGCTGT	CGGAAGCTGT	CCTGCGGGGC	CAGGCCCTGT	TGGTCAACTC	TTCCCAGCCG	420
TGGGAGCCCC	TGCAGCTGCA	TGTGGATAAA	GCCGTCAGTG	GCCTTCGCAG	CCTCACCCT	480
CTGCTTCGGG	CTCTGGGAGC	CCAGAAGGAA	GCC			513

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

TCCCCTCCAG	ATGCGGCCCTC	AGCTGCTCCA	CTCCGAACAA	TCACTGCTGA	CACTTTCGCG	60
AAACTCTTCC	GAGTCTACTC	CAATTTCCCTC	CGGGGAAAGC	TGAAGCTGTA	CACAGGGGAG	120
GCCTGCAGGA	CAGGGGACAG	ATGAGGCGGC	GGCTCCCCC	ACCACGCCTC	ATCTGTGACA	180
GCCGAGTCCT	GGAGAGGTAC	CTCTTGGAGG	CCAAGGAGGC	CGAGAATATC	ACGACGGGCT	240
GTGCTGAACA	CTGCAGCTTG	AATGAGAATA	ATCACTGTCC	CAGACACCAA	AGTTAATTTT	300
TATGCCTGGA	AGAGGATGGA	GGTCGGGCAG	CAGGCCGTAG	AAGTCTGGCA	GGGCCTGGCC	360
CTGCTGTCGG	AAGCTGTCTC	GCGGGGCCAG	GCCCTGTTGG	TCAACTCTTC	CCAGCCGTGG	420
GAGCCCCTGC	AGCTGCATGT	GGATAAAGCC	GTCAGTGGCC	TTCGCAGCCT	CACCACTCTG	480
CTTCGGGCTC	TGGGAGCCCA	GAAGGAAGCC	ATC			513

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

CCTCCAGATG	CGGCCTCAGC	TGCTCCACTC	CGAACAATCA	CTGCTGACAC	TTTCCGCAAA	60
CTCTTCCGAG	TCTACTCCAA	TTTCTCCCGG	GGAAAGCTGA	AGCTGTACAC	AGGGGAGGCC	120
TGCAGGACAG	GGGACAGATG	AGGCGGCGGC	TCCCCCACC	ACGCCTCATC	TGTGACAGCC	180
GAGTCCTGGA	GAGGTACCTC	TTGGAGGCCA	AGGAGGCCGA	GAATATCACG	ACGGGCTGTG	240
CTGAACACTG	CAGCTTGAAT	GAGAATAATC	ACTGTCCCAG	ACACCAAAGT	TAATTTCTAT	300
GCCTGGAAGA	GGATGGAGGT	CGGGCAGCAG	GCCGTAGAAG	TCTGGCAGGG	CCTGGCCCTG	360
CTGTCCGAAG	CTGTCTTGGC	GGGCCAGGCC	CTGTTGGTCA	ACTCTTCCCA	GCCGTGGGAG	420
CCCCTGCAGC	TGCATGTGGA	TAAAGCCGTC	AGTGGCCTTC	GCAGCCTCAC	CACCTTGCTT	480
CGGGCTCTGG	GAGCCCAGAA	GGAAGCCATC	TCC			513

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

CCAGATGCGG	CCTCAGCTGC	TCCACTCCGA	ACAATCACTG	CTGACACTTT	CCGCAAACCTC	60
TTCCGAGTCT	ACTCCAATTT	CCTCCGGGGA	AAGCTGAAGC	TGTACACAGG	GGAGGCCTGC	120
AGGACAGGGG	ACAGATGAGG	CGGCGGCTCC	CCCCACCACG	CCTCATCTGT	GACAGCCGAG	180
TCCTGGAGAG	GTACCTCTTG	GAGGCCAAGG	AGGCCGAGAA	TATCACGACG	GGCTGTGCTG	240
AACACTGCAG	CTTGAATGAG	AATAATCACT	GTCCCAGACA	CCAAAGTTAA	TTTCTATGCC	300
TGGAAGAGGA	TGGAGGTCGG	GCAGCAGGCC	GTAGAAGTCT	GGCAGGGCCT	GGCCCTGCTG	360
TCGGAAGCTG	TCCTGCGGGG	CCAGGCCCTG	TTGGTCAACT	CTTCCCAGCC	GTGGGAGCCC	420
CTGCAGCTGC	ATGTGGATAA	AGCCGTCAGT	GGCCTTCGCA	GCCTCACCAC	TCTGCTTCGG	480
GCTCTGGGAG	CCCAGAAGGA	AGCCATCTCC	CCT			513

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

GATGCGGCCT	CAGCTGCTCC	ACTCCGAACA	ATCACTGCTG	ACACTTTCCG	CAAACTCTTC	60
CGAGTCTACT	CCAATTTCTT	CCGGGGAAAG	CTGAAGCTGT	ACACAGGGGA	GGCCTGCAGG	120
ACAGGGGACA	GATGAGGCGG	CGGCTCCCCC	CACCACGCCT	CATCTGTGAC	AGCCGAGTCC	180
TGGAGAGGTA	CCTCTTGAG	GCCAAGGAGG	CCGAGAATAT	CACGACGGGC	TGTGCTGAAC	240
ACTGCAGCTT	GAATGAGAAT	AATCACTGTC	CCAGACACCA	AAGTTAATTT	CTATGCCTGG	300
AAGAGGATGG	AGGTCGGGCA	GCAGGCCGTA	GAAGTCTGGC	AGGGCCTGGC	CCTGTGTGTC	360
GAAGCTGTCC	TGCGGGGCCA	GGCCCTGTTG	GTCAACTCTT	CCCAGCCGTG	GGAGGCCCTG	420
CAGTGCATG	TGGATAAAGC	CGTCAGTGGC	CTTCGCAGCC	TCACCACTCT	GCTTCGGGCT	480
CTGGGAGCCC	AGAAGGAAGC	CATCTCCCT	CCA			513

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

GCGGCCTCAG	CTGCTCCACT	CCGAACAATC	ACTGCTGACA	CTTTCCGCAA	ACTCTTCCGA	60
GTCTACTCCA	ATTTCTCCG	GGGAAAGCTG	AAGCTGTACA	CAGGGGAGGC	CTGCAGGACA	120
GGGACAGAT	GAGGCGGCGG	CTCCCCCAC	CACGCCTCAT	CTGTGACAGC	CGAGTCTTGG	180
AGAGGTACCT	CTTGGAGGCC	AAGGAGGCCG	AGAATATCAC	GACGGGCTGT	GCTGAACT	240
GCAGCTTGAA	TGAGATAAAT	CACTGTCCCA	GACACCAAAG	TTAATTTCTA	TGCCTGGAAG	300
AGGATGGAGG	TCGGGCAGCA	GGCCGTAGAA	GTCTGGCAGG	GCCTGGCCCT	GCTGTGCGAA	360
GCTGTCTTGC	GGGGCCAGGC	CCTGTTGGTC	AACTCTTCCC	AGCCGTGGGA	GCCCCGTCAG	420
CTGCATGTGG	ATAAAGCCGT	CAGTGGCCTT	CGCACTCTCA	CCACTCTGCT	TCGGGCTCTG	480
GGAGCCCAGA	AGGAAGCCAT	CTCCCCCTCA	GAT			513

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

GCCTCAGCTG	CTCCACTCCG	AACAATCACT	GCTGACACTT	TCCGCAAACCT	CTTCCGAGTC	60
TACTCCAATT	TCCTCCGGGG	AAAGCTGAAG	CTGTACACAG	GGGAGGCCTG	CAGGACAGGG	120
GACAGATGAG	GCGGCGGCTC	CCCCACCCAC	GCCTCATCTG	TGACAGCCGA	GTCTTGAGAG	180
GGTACCTCTT	GGAGGCCAAG	GAGGCCGAGA	ATATCACGAC	GGGCTGTGCT	GAACACTGCA	240
GCTTGAATGA	GAATAATCAC	TGTCCCAGAC	ACCAAAGTTA	ATTTCTATGC	CTGGAAGAGG	300
ATGGAGGTCG	GGCAGCAGGC	CGTAGAAGTC	TGGCAGGGCC	TGGCCCTGCT	GTCCGGAAGCT	360
GTCTGCGGG	GCCAGGCCCT	GTTGGTCAAC	TCTTCCCAGC	CGTGGGAGCC	CCTGCAGCTG	420
CATGTGGATA	AAGCCGTCAG	TGGCCTTCGC	AGCCTCACCA	CTCTGCTTCG	GGCTCTGGGA	480
CCCCAGAAGG	AAGCCATCTC	CCCTCCAGAT	GCG			513

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

TCAGCTGCTC	CACTCCGAAC	AATCACTGCT	GACACTTTCC	GCAAACCTCTT	CCGAGTCTAC	60
TCCAATTTCC	TCCGGGGAAG	GCTGAAGCTG	TACACAGGGG	AGGCCTGCAG	GACAGGGGAC	120
AGATGAGGCG	GCGGCTCCCC	CCACCACGCC	TCATCTGTGA	CAGCCGAGTC	CTGGAGAGGT	180
ACCTCTTGGA	GGCCAAGGAG	GCCGAGAATA	TCACGACGGG	CTGTGCTGAA	CACTGCAGCT	240
TGAATGAGAA	TAATCACTGT	CCCAGACACC	AAAGTTAATT	TCTATGCCTG	GAAGAGGATG	300
GAGGTGCGGC	AGCAGGCCGT	AGAAGTCTGG	CAGGGCCTGG	CCCTGCTGTC	GGAAGCTGTC	360
CTGCGGGGCC	AGGCCCTGTT	GGTCAACTCT	TCCCAGCCGT	GGGAGCCCCCT	GCAGCTGCAT	420
GTGGATAAAG	CCGTCACTGG	CCTTCGCAGC	CTCACCCTC	TGCTTCGGGC	TCTGGGAGCC	480
CAGAAGGAAG	CCATCTCCCC	TCCAGATGCG	GCC			513

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

GCTGCTCCAC	TCCGAACAAT	CACTGCTGAC	ACTTTCCGCA	AACTCTTCCG	AGTCTACTCC	60
AATTTCTCTC	GGGGAAAGCT	GAAGCTGTAC	ACAGGGGAGG	CCTGCAGGAC	AGGGGACAGA	120
TGAGGCGGCG	GCTCCCCCA	CCACGCCTCA	TCTGTGACAG	CCGAGTCCTG	GAGAGGTACC	180
TCTTGAGGCG	CAAGGAGGCC	GAGAATATCA	CGACGGGCTG	TGCTGAACAC	TGCAGCTTGA	240
ATGAGAATAA	TCACTGTCCC	AGACACCAAA	GTTAATTTCT	ATGCCTGGAA	GAGGATGGAG	300
GTGCGGCAGC	AGGCCGTAGA	AGTCTGGCAG	GGCCTGGCCC	TGCTGTGCGA	AGCTGTCTCTG	360
CGGGGCCAGG	CCCTGTTGGT	CAACTCTTCC	CAGCCGTGGG	AGCCCCTGCA	GCTGCATGTG	420
GATAAAGCCG	TCACTGGCCT	TCGCAGCCTC	ACCACCTGTC	TTCGGGCTCT	GGGAGCCCAG	480
AAGGAAGCCA	TCTCCCTCTC	AGATGCGGCC	TCA			513

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

GCTCCACTCC	GAACAATCAC	TGCTGACACT	TTCCGCAAAC	TCTTCCGAGT	CTACTCCAAT	60
TTCTCCGGG	GAAAGCTGAA	GCTGTACACA	GGGGAGGCCT	GCAGGACAGG	GGACAGATGA	120
GGCGGCGGCT	CCCCCACCA	CGCCTCATCT	GTGACAGCCG	AGTCCTGGAG	AGGTACCTCT	180
TGGAGGCCAA	GGAGGCCGAG	AATATCACGA	CGGGCTGTGC	TGAACACTGC	AGCTTGAATG	240
AGAATAATCA	CTGTCCCAGA	CACCAAAGTT	AATTTCTATG	CCTGGAAGAG	GATGGAGGTC	300
GGGCAGCAGG	CCGTAGAAGT	CTGGCAGGGC	CTGGCCCTGC	TGTCGGAAGC	TGTCCTGCGG	360
GGCCAGGCC	TGTTGGTCAA	CTCTTCCCAG	CCGTGGGAGC	CCCTGCAGCT	GCATGTGGAT	420
AAAGCCGTCA	GTGGCCTTCG	CAGCCTCACC	ACTCTGCTTC	GGGCTCTGGG	AGCCCAGAAG	480
GAAGCCATCT	CCCCCTCAGA	TGCGGCCTCA	GCT			513

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

CCACTCCGAA	CAATCACTGC	TGACACTTTC	CGCAAACCTCT	TCCGAGTCTA	CTCCAATTTT	60
CTCCGGGGAA	AGCTGAAGCT	GTACACAGGG	GAGGCCTGCA	GGACAGGGGA	CAGATGAGGC	120
GGCGGCTCCC	CCCACCACGC	CTCATCTGTG	ACAGCCGAGT	CCTGGAGAGG	TACCTCTTGG	180
AGGCCAAGGA	GGCCGAGAAT	ATCACGACGG	GCTGTGCTGA	AACTGTCAGC	TTGAATGAGA	240
ATAATCACTG	TCCCAGACAC	CAAAGTTAAT	TTCTATGCCT	GGAAGAGGAT	GGAGGTCGGG	300
CAGCAGGCCG	TAGAAGTCTG	GCAGGGCCTG	GCCCTGCTGT	CGGAAGCTGT	CCTGCGGGGC	360
CAGGCCCTGT	TGGTCAACTC	TTCCCAGCCG	TGGGAGCCCC	TGCAGCTGCA	TGTGGATAAA	420
GCCGTCAGTG	GCCTTCGCAG	CCTCACCCT	CTGCTTCGGG	CTCTGGGAGC	CCAGAAGGAA	480
GCCATCTCCC	CTCCAGATGC	GGCCTCAGCT	GCT			513

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

CTCCGAACAA	TCAGTGTGA	CACTTTCCGC	AAACTCTTCC	GAGTCTACTC	CAATTTCCCTC	60
CGGGGAAAGC	TGAAGCTGTA	CACAGGGGAG	GCCTGCAGGA	CAGGGGACAG	ATGAGGCGGC	120
GGCTCCCCC	ACCACGCCTC	ATCTGTGACA	GCCGAGTCCT	GGAGAGGTAC	CTCTTGGAGG	180
CCAAGGAGGC	CGAGAAATATC	ACGACGGGCT	GTGCTGAACA	CTGCAGCTTG	AATGAGAATA	240
ATCACTGTCC	CAGACACCAA	AGTTAATTTT	TATGCCTGGA	AGAGGATGGA	GGTCGGGCAG	300
CAGGCCGTAG	AAGTCTGGCA	GGGCCTGGCC	CTGTGTCTCG	AAGCTGTCTT	GCGGGGCCAG	360
GCCCTGTTGG	TCAACTCTTC	CCAGCCGTGG	GAGCCCTGTC	AGCTGCATGT	GGATAAAGCC	420
GTCAGTGGCC	TTCCGACGCT	CACCACTCTG	CTTCGGGCTC	TGGGAGCCCA	GAAGGAAGCC	480
ATCTCCCCCTC	CAGATGCGGC	CTCAGCTGCT	CCA			513

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

CGAACAATCA	CTGCTGACAC	TTTCCGCAA	CTCTTCCGAG	TCTACTCAA	TTTCCTCCGG	60
GGAAAGCTGA	AGCTGTACAC	AGGGGAGGCC	TGCAGGACAG	GGGACAGATG	AGGCGGCGGC	120
TCCCCCACC	ACGCCTCATC	TGTGACAGCC	GAGTCCTGGA	GAGGTACCTC	TTGGAGGCCA	180
AGGAGGCCGA	GAATATCACG	ACGGGCTGTG	CTGAACACTG	CAGCTTGAAT	GAGAATAATC	240
ACTGTCCCAG	ACACCAAAGT	TAATTTCTAT	GCCTGGAAGA	GGATGGAGGT	CGGGCAGCAG	300
GCCGTAGAAG	TCTGGCAGGG	CCTGGCCCTG	CTGTGCGAAG	CTGTCCTGCG	GGGCCAGGCC	360
CTGTTGGTCA	ACTCTTCCCA	GCCGTGGGAG	CCCCTGCAGC	TGCATGTGGA	TAAAGCCGTC	420
AGTGGCCTTC	GCAGCTCAC	CACTCTGCTT	CGGGCTCTGG	GAGCCCAGAA	GGAAGCCATC	480
TCCCCTCCAG	ATGCGGCCTC	AGCTGCTCCA	CTC			513

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

ACAATCACTG	CTGACACTTT	CCGCAAATC	TTCCGAGTCT	ACTCCAATTT	CCTCCGGGGA	60
AAGCTGAAGC	TGTACACAGG	GGAGGCCTGC	AGGACAGGGG	ACAGATGAGG	CGGCGGCTCC	120
CCCCACCACG	CCTCATCTGT	GACAGCCGAG	TCCTGGAGAG	GTACCTCTTG	GAGGCCAAGG	180
AGGCCGAGAA	TATCACGACG	GGCTGTGCTG	AACACTGCAG	CTTGAATGAG	AATAATCACT	240
GTCCAGACA	CCAAAGTTAA	TTTCTATGCC	TGGAAGAGGA	TGGAGGTCGG	GCAGCAGGCC	300
GTAGAAGTCT	GGCAGGGCCT	GGCCCTGCTG	TCGGAAGCTG	TCCTGCGGGG	CCAGGCCCTG	360
TTGGTCAACT	CTTCCCAGCC	GTGGGAGCCC	CTGCAGCTGC	ATGTGGATAA	AGCCGTCAGT	420
GGCCTTCGCA	GCCTCACCAC	TCTGCTTCGG	GCTCTGGGAG	CCCAGAAGGA	AGCCATCTCC	480
CCTCCAGATG	CGGCCTCAGC	TGCTCCACTC	CGA			513

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 501 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

GCCCCACCAC	GCCTCATCTG	TGACAGCCGA	GTCTTGAGAG	GGTACCTCTT	GGAGGCCAAG	60
GAGGCCGAGA	ATATCACGAC	GGGCTGTGCT	GAACACTGCA	GCTTGAATGA	GAATATCACT	120
GTCCAGACA	CCAAAGTTAA	TTTCTATGCC	TGGAAGAGGA	TGGAGGTCGG	GCAGCAGGCC	180
GTAGAAGTCT	GGCAGGGCCT	GGCCCTGCTG	TCGGAAGCTG	TCCTGCGGGG	CCAGGCCCTG	240
TTGGTCAACT	CTTCCCAGCC	GTGGGAGCCC	CTGCAGCTGC	ATGTGGATAA	AGCCGTCAGT	300
GGCCTTCGCA	GCCTCACCAC	TCTGCTTCGG	GCTCTGGGAG	CCCAGAAGGA	AGCCATCTCC	360
CCTCCAGATG	CGGCCTCAGC	TGCTCCACTC	CGAACAATCA	CTGCTGACAC	TTTCCGCAA	420
CTCTTCCGAG	TCTACTCAA	TTTCCTCCGG	GGAAAGCTGA	AGCTGTACAC	AGGGGAGGCC	480
TGCAGGACAG	GGGACAGATG	A				501

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 amino acids
(B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

Ala	Pro	Pro	Arg	Leu	Ile	Cys	Asp	Ser	Arg	Val	Leu	Glu	Arg	Tyr	Leu
1				5				10						15	
Leu	Glu	Ala	Lys	Glu	Ala	Glu	Asn	Ile	Thr	Thr	Gly	Cys	Ala	Glu	His
			20					25					30		
Cys	Ser	Leu	Asn	Glu	Asn	Ile	Thr	Val	Pro	Asp	Thr	Lys	Val	Asn	Phe
		35					40					45			
Tyr	Ala	Trp	Lys	Arg	Met	Glu	Val	Gly	Gln	Gln	Ala	Val	Glu	Val	Trp
	50					55					60				
Gln	Gly	Leu	Ala	Leu	Leu	Ser	Glu	Ala	Val	Leu	Arg	Gly	Gln	Ala	Leu
65					70					75					80
Leu	Val	Asn	Ser	Ser	Gln	Pro	Trp	Glu	Pro	Leu	Gln	Leu	His	Val	Asp
			85						90					95	
Lys	Ala	Val	Ser	Gly	Leu	Arg	Ser	Leu	Thr	Thr	Leu	Leu	Arg	Ala	Leu
		100						105					110		
Gly	Ala	Gln	Lys	Glu	Ala	Ile	Ser	Pro	Pro	Asp	Ala	Ala	Ser	Ala	Ala
		115					120				125				
Pro	Leu	Arg	Thr	Ile	Thr	Ala	Asp	Thr	Phe	Arg	Lys	Leu	Phe	Arg	Val
	130					135					140				
Tyr	Ser	Asn	Phe	Leu	Arg	Gly	Lys	Leu	Lys	Leu	Tyr	Thr	Gly	Glu	Ala
145				150						155					160
Cys	Arg	Thr	Gly	Asp	Arg										
				165											

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 170 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

Thr	Val	Pro	Asp	Thr	Lys	Val	Asn	Phe	Tyr	Ala	Trp	Lys	Arg	Met	Glu
1				5					10					15	
Val	Gly	Gln	Gln	Ala	Val	Glu	Val	Trp	Gln	Gly	Leu	Ala	Leu	Leu	Ser
			20					25					30		
Glu	Ala	Val	Leu	Arg	Gly	Gln	Ala	Leu	Leu	Val	Asn	Ser	Ser	Gln	Pro
		35					40					45			
Trp	Glu	Pro	Leu	Gln	Leu	His	Val	Asp	Lys	Ala	Val	Ser	Gly	Leu	Arg
	50					55					60				
Ser	Leu	Thr	Thr	Leu	Leu	Arg	Ala	Leu	Gly	Ala	Gln	Lys	Glu	Ala	Ile
65					70					75					80
Ser	Pro	Pro	Asp	Ala	Ala	Ser	Ala	Ala	Pro	Leu	Arg	Thr	Ile	Thr	Ala
			85						90					95	
Asp	Thr	Phe	Arg	Lys	Leu	Phe	Arg	Val	Tyr	Ser	Asn	Phe	Leu	Arg	Gly
		100						105					110		
Lys	Leu	Lys	Leu	Tyr	Thr	Gly	Glu	Ala	Cys	Arg	Thr	Gly	Asp	Arg	Gly
		115					120					125			
Gly	Gly	Ser	Ala	Pro	Pro	Arg	Leu	Ile	Cys	Asp	Ser	Arg	Val	Leu	Glu
	130					135					140				
Arg	Tyr	Leu	Leu	Glu	Ala	Lys	Glu	Ala	Glu	Asn	Ile	Thr	Thr	Gly	Cys
145				150						155					160
Ala	Glu	His	Cys	Ser	Leu	Asn	Glu	Asn	Ile						
				165					170						

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

Gly Gly Gly Ser
1

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

Gly Gly Gly Ser Gly Gly Gly Ser
1 5

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

Ser Gly Gly Ser Gly Gly Ser
1 5

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

Glu Phe Gly Asn Met
1 5

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

Glu Phe Gly Gly Asn Met
1 5

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

Glu Phe Gly Gly Asn Gly Gly Asn Met
1 5

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

Gly Gly Ser Asp Met Ala Gly
1 5

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

GCGCGCCCAT GGACAATCAC TGCTGAC

27

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

TCTGTCCCCT GTCCT

15

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

GCGCGCAAGC TTATTATCGG AGTGGAGCAG CTGAGGCCGC ATC

43

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

GCCCCACCAC GCCTCATCTG T

21

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 501 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

TCATCTGTCC	CCTGTCTGTC	AGGCCTCCCC	TGTGTACAGC	TTCAGCTTTC	CCCGGAGGAA	60
ATTGGAGTAG	ACTCGGAAGA	GTTTGCGGAA	AGTGTACAGC	GTGATTGTTC	GGAGTGGAGC	120
AGCTGAGGCC	GCATCTGGAG	GGGAGATGGC	TTCTTCTTGG	GCTCCCAGAG	CCCGAAGCAG	180
AGTGGTGAGG	CTGCGAAGGC	CACTGACGGC	TTTATCCACA	TGCAGCTGCA	GGGGCTCCCA	240
CGGCTGGGAA	GAGTTGACCA	ACAGGGCCTG	GCCCCGCAGG	ACAGCTTCCG	ACAGCAGGGC	300
CAGGCCCTGC	CAGACTTCTA	CGGCCTGCTG	CCCCGACCTC	ATCCTCTTCC	AGGCATAGAA	360

A
ATTAAC TTG GTGTCTGGGA CAGTGATATT CTCATTCAAG CTGCAGTGTT CAGCACAGCC 420
CGTCGTGATA TTCTCGGCCT CCTTGGCCTC CAAGAGGTAC CTCTCCAGGA CTCGGCTGTC 480
ACAGATGAGG CGTGGTGGGG C 501

500-100
100-100
100-100